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OM protein - protein search, using sw model

Run on: December 13, 2004, 17:35:08 ; Search time 154 Seconds
(without alignments)
805.976 Million cell updates/sec

Title: us-09-980-049-1

Perfect score: 1788
Sequence: 1 MERKFSLOPSTISVSEMEPN.....KATKCVFVSWLRKTRV 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1788	100.0	346	4 AAB73097	Aab73097 Human LTC
2	1788	100.0	346	4 AAE07538	Aae07538 Human G-P
3	1788	100.0	346	4 AAU07294	Aau07294 Cyte1ny1
4	1788	100.0	346	4 AAB82852	Aab82852 Human P2Y
5	1788	100.0	346	4 AAU04368	Aau04368 Human G-P
6	1788	100.0	346	4 AAE12022	Aae12022 Human G-P
7	1788	100.0	346	5 AAE12231	Aae12231 Human Cys
8	1788	100.0	346	5 AAG77965	Aag77965 Human G-P
9	1788	100.0	346	5 ABP95624	Abp95624 Human GPC
10	1788	100.0	346	5 ABG66884	Abg66884 Human nov
11	1788	100.0	346	5 ABB05229	Abb05229 Human LTD
12	1788	100.0	346	5 AAU10004	Aau10004 Human Cys
13	1788	100.0	346	6 ABU11923	Abu11923 Human G-P
14	1788	100.0	346	6 ABR81707	Abp81707 Human Cys
15	1788	100.0	346	7 ADH00945	Adh00945 Human Cys
16	1788	100.0	346	7 ADL96460	Adl96460 Human G-P
17	1788	100.0	346	7 ADK51004	Adk51004 Human NOV
18	1788	100.0	346	7 ADK51002	Adk51002 Human NOV
19	1788	100.0	346	8 ADG32520	Adg32520 Human Cys
20	1788	100.0	346	8 ADH41891	Adh41891 Novel hum
21	1788	100.0	346	8 ADH41889	Adh41889 Novel hum
22	1788	100.0	346	8 ADO29277	Ado29277 Human GPC
23	1784	99.8	346	8 ADG25233	Adg25233 Human Cys
24	1782	99.7	346	4 AAU04383	Aau04383 Human G-P
25	1782	99.7	346	7 ADL96534	Adl96534 Human mut

26	1779	99.5	346	4 AAE08553	Aae08553 Human G-P
27	1762	98.5	341	4 AAE07539	Aae07539 Human G-P
28	1762	98.5	341	6 ABU11939	Abu11939 Human G-P
29	1749.5	97.8	347	4 AAB85094	Aab85094 Human Cys
30	1712	95.7	330	5 AAG77964	Aag77964 Human G-P
31	1712	95.7	330	6 ABU11900	Abu11900 Human G-P
32	1673.5	93.6	331	4 AAB85097	Aab85097 Truncated
33	1590	88.9	308	6 ABU11962	Abu11962 Human HGP
34	1516	84.8	253	6 ABU11963	Abu11963 Human HGP
35	1427.5	79.8	309	8 AAB73098	Aab73098 Pig LTC4
36	1197	66.9	309	8 ADO29278	Ado29278 Mouse GPC
37	1187	66.4	309	4 AAB73099	Aab73099 Rat LTC4
38	1187	66.4	309	4 AAB85095	Aab85095 Rat CysLT
39	612	34.2	126	4 AAM25841	Aam25841 Human pro
40	560	31.3	352	8 ADO29276	Ado29276 Mouse GPC
41	559	31.3	337	2 AAW75799	Aaw75799 Human 7-L
42	559	31.3	337	2 AAM65047	Aam65047 A human 7
43	559	31.3	337	4 AAE02492	Aae02492 Human CON
44	559	31.3	337	4 AAB85096	Aab85096 Human Cys
45	559	31.3	337	6 ABU11904	Abu11904 Human Cys

ALIGNMENTS

RESULT 1	
AA73097	AA73097 standard; protein; 346 AA.
ID	AA73097
AC	AA73097;
XX	
DT	05-JUN-2001 (first entry)
XX	
DE	Human LTC4 receptor SEQ ID NO: 2.
XX	
KM	Human; peptide leukotriene receptor; LTC4; allergy;
KW	inflammatory disorder.
XX	
OS	Homo sapiens.
XX	
PN	WO200119986-A1.
XX	
PD	22-MAR-2001.
XX	
PF	13-SEP-2000; 2000WO-JP06265.
XX	
PR	14-SEP-1999; 99JP-00259986.
XX	
PA	(YAMA) YAMANOUCHI PHARM CO LTD.
PA	(HELI-) HELIX RES INST.
XX	
PI	Takasaki J, Kamohara M, Matsumoto M, Saito T, Sugimoto T, Oka T;
PI	Iogaki T, Nishikawa T, Kawai Y;
XX	
DR	WPI; 2001-244800/25.
DR	N-PSDB; AAF81528.
XX	
PT	New leukotriene C4 receptor protein for screening modifiers of ligand
PT	binding activity for treating allergic and inflammatory disorders, such
PT	as ulcerative colitis and asthma.
XX	
PS	Claim 1; Page 63-64; 83pp; Japanese.
XX	
CC	The present invention provides the protein and coding sequences of a
CC	novel human, pig and rat leukotriene C4 receptor. These sequences can be
CC	used to screen for substances that can be used in the treatment and
CC	prevention of allergic and inflammatory disorders including dermatitis,
CC	inflammatory bowel disease, ulcerative colitis, asthma and bronchitis.
CC	The present sequence is the human LTC4 receptor
XX	
SQ	Sequence 346 AA;
Query Match	100.0%; Score 1788; DB 4; Length 346;

Best Local Similarity 100.0%; Pred. No. 2.7e-180;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MERKFMISLOPSISVSSEMEPNGTFSNNNSNCTIENFKREPPYVYLIIFFWGLANGLSI 60
DB 1 MERKFMISLOPSISVSSEMEPNGTFSNNNSNCTIENFKREPPYVYLIIFFWGLANGLSI 60
QY 61 YVFLQPYKSTSVNFMNLAIISDLPISTLPFRADYLRGSNMIFGDLACRIMSISLYV 120
DB 61 YVFLQPYKSTSVNFMNLAIISDLPISTLPFRADYLRGSNMIFGDLACRIMSISLYV 120
QY 121 NMTSSIFLTVLSVVRFLAMVHPRLIHTSIRSAMIICGIIWILIMASSIMLDSGSEQ 180
DB 121 NMTSSIFLTVLSVVRFLAMVHPRLIHTSIRSAMIICGIIWILIMASSIMLDSGSEQ 180
QY 181 NSGVTSCLEMLNFKIKAKQTMNYIALVVGCLPFTLSICYLLIIRVLKVEVPSGLRV 240
DB 181 NSGVTSCLEMLNFKIKAKQTMNYIALVVGCLPFTLSICYLLIIRVLKVEVPSGLRV 240
QY 241 SHRKALTTIIITLIIFFLCPLPYHTLRVHTLTKWVGLCKDRLHKALVITLALAAANCF 300
DB 241 SHRKALTTIIITLIIFFLCPLPYHTLRVHTLTKWVGLCKDRLHKALVITLALAAANCF 300
QY 301 NPLIYFAGENFKORLKSALRKGPQAKTKCVFPVSVMLRKETRV 346
DB 301 NPLIYFAGENFKORLKSALRKGPQAKTKCVFPVSVMLRKETRV 346

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RESULT 2

AAE07538 standard; protein; 346 AA.

AAE07538;

06-NOV-2001 (first entry)

Human G-protein coupled receptor 1a (GPCR1a) variant.

Human; G-protein coupled receptor; GPCR; GPCR1a; cardiomyopathy;
atherosclerosis; hypertension; congenital heart defect; anorexia;
atrial septal defect; ventricular septal defect; valve disease;
scleroderma; obesity; transplantation; adrenoleucodystrophy; AIDS;
congenital adrenal hyperplasia; prostate cancer; lymphoma; cancer;
haemophilia; idiopathic thrombocytopenic purpura; dyslipidaemia;
acquired immune deficiency syndrome; diabetes; infectious disease;
metabolic syndrome X; Albright Hereditary Osteodystrophy; ASD; VSD;
neurodegenerative disorder; Alzheimer's disease; immune disorder;
fertility; Parkinson's disorder; haematopoietic disorder.

Homo sapiens.

Key Location/Qualifiers

Peptide 1..59 /label= Signal_peptide

Protein 60..346 /label= Mature_human_GPCR1a_protein_variant

MO200159113-A2.

16-AUG-2001.

08-FEB-2001; 2001MO-US004404.

08-FEB-2000; 2000US-0180929P.

09-FEB-2000; 2000US-0181045P.

09-FEB-2000; 2000US-0181339P.

09-FEB-2000; 2000US-0181344P.

17-FEB-2000; 2000US-0183392P.

20-JUL-2000; 2000US-0219585P.

20-JUL-2000; 2000US-0219758P.

26-JUL-2000; 2000US-0221341P.

XX (CURA-) CURAGEN CORP.
XX Taupier RJ, Burgess CE, Padigaru M, Tchernev VT, Mishra VS;
PI Casman S, Ballinger R, Vernet CAM, Li L, Spytek KA, Andrew DP;
PI Mezes PS;
XX
XX MPI: 2001-497077/54.
DR N-PSDB; AAD13709.

PT Novel G-protein coupled receptor proteins (GPCR1-GPCR-7) useful for
PT treating or preventing, e.g., cardiomyopathy, atherosclerosis,
PT hypertension, acquired immune deficiency syndrome, bronchial asthma,
PT Crohn's disease, and multiple sclerosis.

XX Claim 1, Page 6; 135pp; English.

CC The invention relates to human G-protein coupled receptor proteins 1-7
CC (GPCR1-7 or GPCR) and nucleic acid molecules encoding such proteins.
CC GPCR sequences are used to treat or prevent a human suffering from GPCR
CC -associated disorders, e.g. cardiomyopathy, atherosclerosis,
CC hypertension, congenital heart defects, aortic stenosis, atrial septal
CC defect (ASD), atriocentricular (A-V) canal defect, ductus arteriosus,
CC pulmonary stenosis, subaortic stenosis, ventricular septal defect (VSD),
CC valve diseases, tubercular sclerosis, scleroderma, obesity,
CC transplantation, adrenoleucodystrophy, congenital adrenal hyperplasia,
CC prostate cancer, neoplasm, adenocarcinoma, lymphoma, uterine cancer,
CC fertility, haemophilia, hypercoagulation, idiopathic thrombocytopenic
CC purpura, graft versus host disease, acquired immune deficiency syndrome
CC (AIDS), bronchial asthma, Crohn's disease, multiple sclerosis, and
CC treatment of Albinism Hereditary Osteodystrophy. GPCR antibodies are
CC used to treat a pathological state and treat or prevent disorders such as
CC diabetes, metabolic disturbances associated with obesity, metabolic
CC syndrome X, anorexia, wasting disorders associated with chronic diseases,
CC infectious disease, cancer-associated cachexia, cancer, neurodegenerative
CC disorders, Alzheimer's disease, Parkinson's disorder, immune disorders,
CC haematopoietic disorders and various dyslipidaemias. GPCR DNA is also
CC useful in gene therapy. The present sequence is human GPCR1a protein
CC variant

XX SQ Sequence 346 AA;

Query Match 100.0%; Score 1788; DB 4; Length 346;
Best Local Similarity 100.0%; Pred. No. 2.7e-180;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MERKFMISLOPSISVSSEMEPNGTFSNNNSNCTIENFKREPPYVYLIIFFWGLANGLSI 60
DB 1 MERKFMISLOPSISVSSEMEPNGTFSNNNSNCTIENFKREPPYVYLIIFFWGLANGLSI 60
QY 61 YVFLQPYKSTSVNFMNLAIISDLPISTLPFRADYLRGSNMIFGDLACRIMSISLYV 120
DB 61 YVFLQPYKSTSVNFMNLAIISDLPISTLPFRADYLRGSNMIFGDLACRIMSISLYV 120
QY 121 NMTSSIFLTVLSVVRFLAMVHPRLIHTSIRSAMIICGIIWILIMASSIMLDSGSEQ 180
DB 121 NMTSSIFLTVLSVVRFLAMVHPRLIHTSIRSAMIICGIIWILIMASSIMLDSGSEQ 180
QY 181 NSGVTSCLEMLNFKIKAKQTMNYIALVVGCLPFTLSICYLLIIRVLKVEVPSGLRV 240
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QY 241 SHRKALTTIIITLIIFFLCPLPYHTLRVHTLTKWVGLCKDRLHKALVITLALAAANCF 300
DB 241 SHRKALTTIIITLIIFFLCPLPYHTLRVHTLTKWVGLCKDRLHKALVITLALAAANCF 300
QY 301 NPLIYFAGENFKORLKSALRKGPQAKTKCVFPVSVMLRKETRV 346
DB 301 NPLIYFAGENFKORLKSALRKGPQAKTKCVFPVSVMLRKETRV 346

```

RESULT 3

AAU07294

ID AAU07294 standard; protein; 346 AA.
 XX
 AC AAU07294;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Cysteineyl leukotriene receptor HIPHM0000007.
 XX
 KM Cysteineyl leukotriene receptor; HIPHM0000007; antiaesthetic; antihiv;
 KM antiallergic; antiinflammatory; antiarteriosclerotic; antiarrhythmic;
 KM vasotrophic; cytosolic; neuroprotective; antineurotic; antiatherosclerotic;
 KM immunosuppressive; antiparasitic; dermatological; antibacterial;
 KM cerebroprotective; antihypertensive; asthma; allergic rhinitis; AIDS;
 KM cardiac arrhythmia; myocardial ischemia; atherosclerosis; heart failure;
 KM rheumatoid arthritis; immune disorder; dermatitis; septic shock; stroke.
 XX
 OS Homo sapiens.
 XX
 PN WO200159105-A1.
 XX
 PD 16-AUG-2001.
 XX
 PF 12-FEB-2001; 2001WO-GB000560.
 XX
 PR 10-FEB-2000; 2000GB-00003079.
 XX
 PA (GLAXO) GLAXO GROUP LTD.
 XX
 PI Couzens DJ, Volpe F, Ignar DM;
 XX
 DR WPI: 2001-514666/56.
 XX
 DR N-PSDB; AAS10778.
 XX
 PT Novel cysteineyl leukotriene receptor polypeptide, termed as HIPHM0000007
 PT polypeptide, useful for treating cardiovascular diseases, lung diseases,
 PT allergic rhinitis, immune deficiency and disorder.
 XX
 PS Claim 1; Page 47-48; 52pp; English.
 CC The sequence represents the amino acid sequence of cysteineyl leukotriene
 CC receptor polypeptide, termed as HIPHM0000007. The nucleic acid is useful
 CC for identifying a substance that modulates cysteineyl leukotriene receptor
 CC activity. This substance is useful for treating a subject having a
 CC disorder which is responsive to cysteineyl leukotriene receptor
 CC modulation, such as asthma, chronic obstructive pulmonary disease (COPD),
 CC allergic rhinitis, cardiac arrhythmia, myocardial ischemia,
 CC atherosclerosis and heart failure. It is also useful in the therapeutic
 CC treatment and/or prophylaxis of disorders such as acquired immune
 CC deficiency syndrome (AIDS), rheumatoid arthritis, multiple sclerosis,
 CC leukemia, myasthenia gravis, Grave's disease, systemic lupus
 CC erythematosus, inflammatory bowel disease, encephalomyelitis, psoriasis,
 CC atopic dermatitis, septic shock, stroke and ischemia reperfusion injury.
 CC The antibody to cysteineyl leukotriene receptor is useful for
 CC immunoprecipitation techniques, as tools to further elucidate the
 CC function of HIPHM0000007 or its variant, and as therapeutic agent. The
 CC nucleic acid is useful for identifying mutations in HIPHM0000007 gene
 CC implicated in human disorders, which is in turn useful for diagnosing the
 CC disorder or susceptibility to the disorder and in assessing the
 CC physiology of the disorders. It is also useful in hybridisation studies
 CC to monitor up- or down-regulation of HIPHM0000007 expression
 XX
 SQ Sequence 346 AA;
 Query Match 100.0%; Score 1788; DB 4; Length 346;
 Best Local Similarity 100.0%; Pred. No. 2, 7e-180;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 MERKFMLOPSISSEMEPPCTPSNNRNCTIENFKRGEPPPIYLLIFWGVLTGKSLT 60
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 DB 61 YVFLQPKKSTSVNFMNLNLAISDLLFISTLPFRADYYLRGSMWIFGDLACRIMSSTLYV 120

DB 61 YVFLQPKKSTSVNFMNLNLAISDLLFISTLPFRADYYLRGSMWIFGDLACRIMSSTLYV 120
 QY 121 NMTSSIFLTLSVVRFLAVHPFRLHTSISANILGIIWILMASSIMLDSGSEQ 180
 DB 121 NMTSSIFLTLSVVRFLAVHPFRLHTSISANILGIIWILMASSIMLDSGSEQ 180
 QY 181 NGSVTSCEINLYKIKLQTMNYIALVGCILPPFTLSICVLLITVILKVEVPEGSLRV 240
 DB 181 NGSVTSCEINLYKIKLQTMNYIALVGCILPPFTLSICVLLITVILKVEVPEGSLRV 240
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 DB 241 SHRKALTTITITLIFPLCPYHTLRTVHLATWKGCLCKDRHLKALVITLAAANACP 300
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 DB 301 NPLLYYPAGENFKDRKLSALRKGPQKATKCVFVSVLKRKTRV 346
 RESULT 4
 AAB82852
 ID AAB82852 standard; protein; 346 AA.
 XX
 AC AAB82852;
 XX
 DT 12-NOV-2001 (first entry)
 XX
 DE Human P2Y-1like GPCR protein.
 XX
 KM P2Y-1like; G-protein coupled receptor; GPCR; human;
 KM cysteineyl leukotriene receptor; cycLTL LTD4; bactericide; fungicide;
 KM protozoacide; virucide; analgesic; cytosolic; anabolic; antiaesthetic;
 KM antiparkinsonian; cardiac; hypertensive; hypotensive; osteopathic;
 KM anticancer; immunosuppressive; antiallergic; antisclerotic;
 KM neuroprotective; antipsychotic; therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Location/Qualifiers
 FT 41..63
 FT /label= TM1
 FT /note= "transmembrane domain 1"
 FT 77..96
 FT /label= TM2
 FT /note= "transmembrane domain 2"
 FT 114..137
 FT /label= TM3
 FT /note= "transmembrane domain 3"
 FT 156..173
 FT /label= TM4
 FT /note= "transmembrane domain 4"
 FT 202..223
 FT /label= TM5
 FT /note= "transmembrane domain 5"
 FT 249..266
 FT /label= TM6
 FT /note= "transmembrane domain 6"
 FT 296..313
 FT /label= TM7
 FT /note= "transmembrane domain 7"
 FT
 PN WO200168842-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 13-MAR-2001; 2001WO-BE002785.
 XX
 PR 14-MAR-2000; 2000US-0189045P.
 XX
 PA (PARB) BAYER AG.
 XX
 PI Xiao Y;
 XX

Db 181 NGSVTSCLSLNLYKIALQTMNIALVVGCLPFTLSICYLIIIRVLKVEVPSGLRV 240
 QY 241 SHRRALTTIIITIIIFLFCFLPYHTLRTVHLTWKVGCDRLKALVITLALAAANACF 300
 Db 241 SHRRALTTIIITIIIFLFCFLPYHTLRTVHLTWKVGCDRLKALVITLALAAANACF 300
 QY 301 NPLLYYFAGENFDRKLSALRKGPQAKTKCVFVSWMLRKETRV 346
 Db 301 NPLLYYFAGENFDRKLSALRKGPQAKTKCVFVSWMLRKETRV 346
 RESULT 6
 ID AAE12022 standard; protein; 346 AA.
 AC AAE12022;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Human G-protein coupled receptor; GCRC-1.
 XX
 KW Human; G-protein coupled receptor; GCRC; gene therapy;
 KW proteasome analysis; cell proliferative disorder; arteriosclerosis;
 KW cancer; neurological disorder; Huntington's disease; Parkinson's disease;
 KW cardiovascular disorder; atherosclerosis; congestive heart failure;
 KW gastrointestinal disorder; gastritis; nausea; autoimmune; anaemia;
 KW inflammatory disorder; acquired immunodeficiency syndrome; AIDS;
 KW metabolic disorder; diabetes; obesity; viral infection; drug screening;
 KW chromosomal mapping; cytostatic; immunomodulatory; anti-inflammatory;
 KW virucide.
 XX
 OS Homo sapiens.
 XX
 FT Key Location/Qualifiers
 FT Peptide 1..55
 FT /label= signal_peptide
 FT Domain 38..61
 FT /label= Transmembrane_domain
 FT Protein 56..346
 FT /note= "Mature human GCRC-1 protein"
 FT Domain 198..221
 FT /label= Transmembrane_domain
 XX
 FT MO200172836-A2.
 XX
 PD 04-OCT-2001.
 XX
 PF 29-MAR-2001; 2001WC-US010436.
 XX
 PR 29-MAR-2000; 2000US-0193051P.
 PR 06-APR-2000; 2000US-0195155P.
 PR 20-APR-2000; 2000US-0190848P.
 PR 28-APR-2000; 2000US-0200551P.
 PR 05-MAY-2000; 2000US-020278P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 PI Policky JL, Tribouley CM, Tang YT, Baughn MR, Graul R, Khan FA;
 PI Nguyen DB, Patterson C, Lal P, Au-Young J, Yang J, Hatalla A;
 PI Walla NK, Das D;
 XX
 DR WPI, 2001-616472/71.
 XX
 N-PSDB; AAD19577.
 XX
 PT New human G-protein coupled receptors, useful for treatment and diagnosis
 PT of e.g. cell proliferation, also screening for specific modulators, and
 PT related nucleic acid.
 XX
 PS Claim 1, Page 101-102, 11pp; English.
 XX
 CC The present sequence is a human G-protein coupled receptor, GCRC-1
 CC protein. The GCRCs are used for treating or preventing disorders
 CC associated with decreased expression of functional GCRC, and for

CC identifying specific agonists and antagonists, also binding agents and
 CC modulators. They can also be used for generating specific antibodies and
 CC for proteasome analysis. Disorders that can be treated include cell
 CC proliferative disorders, e.g., arteriosclerosis and cancer, neurological
 CC disorders, e.g., Huntington's disease and Parkinson's disease,
 CC cardiovascular disorders, e.g., atherosclerosis and congestive heart
 CC failure, gastrointestinal disorders, e.g., gastritis and nausea,
 CC autoimmune/inflammatory disorders, e.g., acquired immunodeficiency
 CC syndrome (AIDS) and anaemia, metabolic disorders, e.g., diabetes and
 CC obesity and viral infections. Nucleic acids that encode GCRC are used
 CC for identifying agents that alter its expression, for assessing toxicity
 CC of test compounds, and as sources of primers and probes for diagnostic
 CC detection of GCRC DNA and of therapeutic antisense and ribozyme
 CC sequences. They can also be used in gene therapy, for chromosomal
 CC mapping, and for recombinant production of GCRC. The antibodies are
 CC useful for diagnosis and monitoring of diseases associated with GCRC
 CC expression, for detecting and purifying GCRC, and as therapeutic agents
 CC and for drug screening
 XX
 SQ Sequence 346 AA;
 XX
 Query Match 100.0%; Score 1788; DB 4; Length 346;
 Best Local Similarity 100.0%; Pred. No. 2,7e-180;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MERKFMGSLQPSISVSEMEPNGTFSNNNSRNCITENKREFFPIVYLIIFPMGVLAGNLSI 60
 Db 1 MERKFMGSLQPSISVSEMEPNGTFSNNNSRNCITENKREFFPIVYLIIFPMGVLAGNLSI 60
 QY 61 YVFLQPKYSTSVNVMNLAIISDLFIETLPRADYVLRGSWIGDLACRIMSYSLVY 120
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 Db 121 NMTSIVFLTVLSVVFELMVHFRLLHVTISRSAMILGIIWILMASSIMLDSGSEQ 180
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 Db 181 NGSVTSCLSLNLYKIALQTMNIALVVGCLPFTLSICYLIIIRVLKVEVPSGLRV 240
 QY 241 SHRRALTTIIITIIIFLFCFLPYHTLRTVHLTWKVGCDRLKALVITLALAAANACF 300
 Db 241 SHRRALTTIIITIIIFLFCFLPYHTLRTVHLTWKVGCDRLKALVITLALAAANACF 300
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 Db 301 NPLLYYFAGENFDRKLSALRKGPQAKTKCVFVSWMLRKETRV 346
 RESULT 7
 ID AAE17231 standard; protein; 346 AA.
 AC AAE17231;
 XX
 DT 07-MAY-2002 (first entry)
 XX
 DE Human CybL72 GPCR (G-protein coupled receptor).
 XX
 KW Human; CybL72 GPCR; G-protein coupled receptor; oedema; asthma;
 KW immunological disorder; vascular disorder; reproductive disease;
 KW cellular metabolism; growth; development; blood; bone homeostasis;
 KW inflammation; allergy; angiogenesis; respiratory distress syndrome;
 KW Crohn's disease; blood pressure; protein therapy; anti-inflammatory;
 KW inflammatory disorder.
 XX
 OS Homo sapiens.
 XX
 FT Key Location/Qualifiers
 FT Domain 1..41
 FT /label= Extracellular_domain
 FT Modified-site 20..22

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FT      /note= "N-glycosylation site"
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FT      /note= "N-glycosylation site"
FT      94..115
FT      /note= "Extracellular domain between the second and third
FT      transmembrane domains"
FT      175..203
FT      /note= "Extracellular domain between the fourth and fifth
FT      transmembrane domains"
FT      181..183
FT      /note= "N-glycosylation site"
FT      268..289
FT      /note= "Extracellular domain between the sixth and
FT      seventh transmembrane domains"
FT      Domain
FT      Modified-site
FT      181..183
FT      /note= "N-glycosylation site"
FT      268..289
FT      /note= "Extracellular domain between the sixth and
FT      seventh transmembrane domains"
XX      MO200192302-A2.
XX      PD
XX      06-DEC-2001.
XX      PD
XX      25-MAY-2001; 2001WO-US016965.
XX      PF
XX      26-MAY-2000; 2000US-0207725P.
XX      PR
XX      (REG-) REGENERON PHARM INC.
XX      PA
XX      Murphy A, Martin J;
XX      PI
XX      DR      MPI: 2002-154523/20.
XX      N-PSDB; AAD28591.
XX      PS
XX      Claim 2; Fig 1A-1C; 58pp; English.
XX      CC      The invention relates to human CysLT2 GPCR (G-protein coupled receptor)
XX      CC      polypeptide and its corresponding nucleic acid. The human CysLT2 GPCR,
XX      CC      antibodies and compositions are useful for treating the human or animal
XX      CC      body, or for diagnosing a disease. Human CysLT2 GPCR is useful for
XX      CC      diagnosing, preventing and treating inflammatory, immunological, vascular
XX      CC      disorders, reproductive diseases, or diseases related to cellular
XX      CC      metabolism, growth, development, blood and bone homeostasis. These
XX      CC      disorders or diseases include asthma, inflammation, allergy,
XX      CC      angiogenesis, respiratory distress syndrome, Crohn's disease, oedema,
XX      CC      high or low blood pressure growth, development, blood and bone
XX      CC      homeostasis. Human CysLT2 GPCR is also used in protein therapy. The
XX      CC      present sequence is human CysLT2 GPCR protein
XX      SQ      Sequence 346 AA;
SQ      Query Match      100.0%; Score 1788; DB 5; Length 346;
SQ      Best Local Similarity 100.0%; Pred. No. 2,7e-180;
SQ      Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

DB      241 SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTWKVGCKDRLHAKLVITLALAAANACF 300
QY      301 NPLLYYFAGENFKDKLAKRGHPQKATKCVFVSWLRKRETV 346
DB      301 NPLLYYFAGENFKDKLAKRGHPQKATKCVFVSWLRKRETV 346
RESULT 8
AAG77965
ID      AAG77965 standard; protein, 346 AA.
AC      AAG77965;
XX      25-FEB-2002 (first entry)
DT      Human G-protein coupled receptor PFI-017*.
DE      Human G-protein coupled receptor PFI-017*.
XX      Human; G-protein coupled receptor; GPCR; PFI-017*; cytosolic;
XX      antiallergic; osteopathic; cardiovascular; immunosuppressive; neoplastic;
XX      gene therapy; heart disease; gastrointestinal disease; sleep disorder;
XX      immunological disorder; pulmonary disorder; infectious disease;
XX      myeloproliferative disease; allergic rhinitis; asthma; COPD; obesity;
XX      chronic obstructive pulmonary disease; inflammatory bowel disease;
XX      diabetes; metabolic disease; neurological disease; urogenital disease;
XX      inflammation; cancer; osteoporosis; cardiovascular disease; infection;
XX      allergy; respiratory disease; sensory organ disorder; hair loss;
XX      immunological disorder; pulmonary disease; neoplastic disease;
XX      vasculitic granulomatous disease; dermatology; psychotherapeutic.
XX      OS      Homo sapiens.
XX      PN      US2001039037-A1.
XX      PD      08-NOV-2001.
XX      PF      05-APR-2001; 2001US-00826791.
XX      PR      05-APR-2000; 2000GB-00008504.
XX      PR      19-APR-2000; 2000US-0198367P.
XX      PA      (HARL/) HARLAND L.
XX      PI      Harland L;
XX      DR      MPI: 2002-040722/05.
XX      N-PSDB; AAH77279.
XX      PS      Claim 7; Fig 7B; 39pp; English.
XX      CC      The sequence represents a novel G-protein coupled receptor (GPCR), PFI-
XX      CC      017* of the invention. The PFI-017 has cytostatic, antiallergic,
XX      CC      osteopathic, cardiovascular, and immunosuppressive activity. The
XX      CC      polynucleotides may have a use in gene therapy. The polynucleotide is
XX      CC      useful for treating allergic disorders, an inflammatory disorder, an
XX      CC      immunological disorder, a pulmonary disorder, an infectious disease, a
XX      CC      neoplastic or myeloproliferative disease, or a heart disease. The
XX      CC      allergic disorder is an allergic rhinitis or asthma, the pulmonary
XX      CC      disease is COPD, and the inflammatory disorder is inflammatory bowel
XX      CC      disease. PFI-017 polynucleotide sequences may be used for the diagnosis
XX      CC      of diseases resulting from expression of PFI-017, and to detect and
XX      CC      quantify gene expression in conditions, disorders or diseases in which
XX      CC      PFI-017 activity may be implicated. The polypeptides are used to produce
XX      CC      anti-PFI-017 antibodies to be used diagnostically to detect and quantify
XX      CC      PFI-017 levels in disease states. The antibodies, compounds and
XX      CC      compositions which can modulate the peptide can be used in treating
XX      CC      obesity, diabetes and metabolic disease, neurological disease, urogenital
XX      CC      disease, inflammation, cancer, osteoporosis, cardiovascular disease,

```

CC gastrointestinal disease, infections, allergy and respiratory disease,
CC sensory organ disorders, sleep disorders, hair loss, immunological
CC disorders, pulmonary diseases, infectious diseases, neoplastic and
CC myeloproliferative diseases, vasculitic granulomatous diseases, and heart
CC diseases. These may also be used in dermatology, and psychotherapeutics
XX Sequence 346 AA;

SQ Sequence 346 AA;

Query Match	100.0%	Score 1788;	DB 5;	Length 346;
Best Local Similarity	100.0%	Pred. No.	2.7e-180;	
Matches 346;	Conservative	0;	Mismatches	0;
			Indels	0;
			Gaps	0;

```

Qy      1 MERKMSLQPSISVSEMEPNGTFSNNNSRNCITENFKREFPIVYLIIFFWGLGNGLSI 60
          |||||
Db      1 MERKMSLQPSISVSEMEPNGTFSNNNSRNCITENFKREFPIVYLIIFFWGLGNGLSI 60

```

61 YVLPDPYKKSISVNVEMLNLAISDLFIETLPFRADYYLRGSNWIFGLACRIMSYSLV 120

121 NMISLIFLIVLSVVRFLAMVHPRRLHVTLSRSAMILCGIIMLIMASSIMLDDSGEQ 180
 121 NMYSYFLITVLSVRFLAMVHPRRLHVTLSRSAMILCGIIMLIMASSIMLDDSGEQ 180

181 NSSVTSCLBUDNLSAKLQTNMYIALVVGCLPFTLSICYLIIIRVLKVEVPESGRV 240

Db 241 SHRKALTTITLIIFFLCPEYHTARTVHLTTWKVGICKDRHKALVITLALAAANCF 3000

Db 301 NPLYYFAGENFKDRLKSAALRKGHPQAKTKCVFPAVSVMRLKETRV 346

RESULT 9	
ABP95624	
ID	ABP95624 standard; protein; 346 AA.

AC	ABP95624,
XX	
DT	06-MAR-2003 (first entry)

DE Human GPCR polypeptide SEQ ID NO 58.
XX
KW Human; GPCR; G protein coupled receptor; signal transduction; olfactory;

XX
OS Homo sapiens.
XX

XX 28-FEB-2002.
PD
XX
DE 30-JUL-2001, 2001WD-TP001446

AA 04-AUG-2000; 2000JP-00237818.
PR 13-FEB-2001; 2001JP-00034434.
XX

EN (INASC-) OAFAN SCI & TECHNOLOGI CORP.
 XX
 PI Haga T, Takeda S, Mitaku S;
 XX

PT Database global search for G protein-coupled receptors, proteins and

PT	Identifying targets for drug development.
XX	
PS	Claim 10; SEQ ID NO 58; 97pp + Sequence listing; Japanese.

xx The invention relates to a method for screening G protein-coupled
cc receptors (GPCR) genes (AB242870-AB243216) and/or GPCR proteins (ABP95596-
cc AB295962) by extracting open-reading frames containing 6-8 transmembrane
cc domains with 250-1000 amino acid residues to give a gene homologous with
cc a known GPCR gene. The receptor proteins and encoded genes are useful for
cc studying *in vivo* signal transduction mechanism and identifying targets

CC form of agonists and antagonists by screening intrinsic and extrinsic
CC ligands as bitter taste inhibitors, taste enhancers and fragrance
CC improvers. Note: The sequence data for this patent did not form part of

CC from wipo at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 346 AA;

Query Match	100.0%;	Score 1788;	DB 5;	Length 346;
Best Local Similarity	100.0%;	Pred. No. 2,7e-180;		
Matches 346;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Db

CY 1 MERKFMSSLPSSISVSEMEPNNGTISNNNSKNCILIANFKBFFFLVILILFFMGVLGNGPSI 60

1 MERKFMSSLPSSISVSEMEPNNGTISNNNSKNCITENFKBFPPIVYLILFFMGVLGNGPSI 60

61 YVEFQPKKSTSVVFMNLAIISDLLFSTLPADYYLRGSMNI FGDIACRIMSYSLV 120

DB 121 NMYSIYELTVLSVRFPLAMVHPRFLHTVTSIRSAMIIGIITWILIMASSIMLDGSGEQ 180

Db 181 NGSYTSCLELNLYKIAKQTMNIALVVGCLLPFTLSICYLLIRVLLKVEVPSGRV 240

Db. 241 SHKALTTITITITITIFELCELPHILRLVHLITWKVGCCKDRHKALVITLALNANACE 300

Db 301 NPLIYFAGENFKDRLKSAIRKGRPOKAKTKCVFVSVIWLKRETRV 346

RESULT 10
ABG66684
ID ABG66684 standard; protein; 346 AA.

AC	ABG66684;
XX	
DT	30-AUG-2002 (first entry)
ST	

Human novel polypeptide #19.
DIE
XX
KX
KW
Human inflammatory condition; shock; sepsis; immune response; cancer;
novel; health control network; diabetes mellitus

KW parainfluenza nervous system diseases; amyotrophic lateral sclerosis; leucomeningitis
KW myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone; cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; metatarsal disease; revascularization injury

XX
fungal infection.
KW
allergic condition; thrombolysis; coagulation disorder;
KW
fungal infection.
XX

:none :off :on :
 XX
 PN WO200244340-A2.
 XX

XX
XX
XX
30-NOV-2001, 2001WO-US047004.

PR 30-NOV-2000; 2000US-00728952.
XX (HYSE-) HYSEQ INC.
PA Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Wang J, Wang D,
PI Yamazaki V, Ujwal MU, Drmanac RT,
XX MPI; 2002-508509/54.
DR N-PSDB; ABK94908.
XX
PT Novel nucleic acids and polypeptides for diagnosis, treatment of
PT inflammatory, autoimmune, nervous system, myeloid or lymphoid cell
PT disorders, cancer and promoting wound healing.
XX
PS Claim 10; Page 582-583; 672pp; English.
XX
CC The invention relates to human novel polynucleotides and associated
CC polypeptides. The polynucleotides and polypeptides are useful for
CC treating inflammatory conditions such as arthritis, nephritis, Crohn's
CC disease, ischaemia-reperfusion injury, shock, sepsis, immune responses
CC and cancer and for promoting wound healing. The sequences are used to
CC induce the proliferation of neural cells and regeneration of nerve and
CC brain tissue, and are useful for the treatment of central and peripheral
CC nervous system diseases and neuropathies, such as Alzheimer's disease,
CC Parkinson's disease, Huntington's disease and amyotrophic lateral
CC sclerosis. The sequences are involved in chemotactic or chemokinetic
CC activity, regulation of haematopoiesis, treatment of myeloid or lymphoid
CC cell disorders and platelet disorders such as thrombocytopenia,
CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue
CC growth, tissue repair, healing of burns, incisions, ulcers, treatment of
CC osteoporosis, osteoarthritis, bone degenerative disorders and periodontal
CC disease. The sequences of the invention are also useful for gut
CC protection or regeneration and treatment of lung or liver fibrosis,
CC reperfusion injury in various tissues, immune deficiencies and disorders
CC including severe combined immunodeficiency (SCID), bacterial or fungal
CC infections, autoimmune disorders e.g. multiple sclerosis and myasthenia
CC gravis, allergic conditions such as asthma, thrombolytic or thrombotic
CC and coagulation disorders. Sequences ABG6666-ABG66758 represent human
CC novel polypeptides of the invention
XX
XX Sequence 346 AA:

Query Match 100.0%; Score 1788; DB 5; Length 346;
Best Local Similarity 100.0%; Pred. No. 2.7e-180;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MERKPMSTQPSISVSEMEPNGTFSNNRNCTIENFKRPFPIVYLIIFFMGVLNGLSI 60
DB 1 MERKPMSTQPSISVSEMEPNGTFSNNRNCTIENFKRPFPIVYLIIFFMGVLNGLSI 60
QY 61 YVFLQPYKSTSVNVMNLAIISDLFIETLPFRADYLRGSMWIRGDLACRIMSYSLVY 120
DB 61 YVFLQPYKSTSVNVMNLAIISDLFIETLPFRADYLRGSMWIRGDLACRIMSYSLVY 120
QY 121 NMYSSTYFLTVLSVAFELAMVHPFRLLHVTISRANILGIIWILIMASSIMLDGSGSQ 180
DB 121 NMYSSTYFLTVLSVAFELAMVHPFRLLHVTISRANILGIIWILIMASSIMLDGSGSQ 180
QY 181 NSQSVSCLELNYKIAKQTMNYIALVGCCLPFFLTSLCYLLIIRVLLKVEPESGLRV 240
DB 181 NSQSVSCLELNYKIAKQTMNYIALVGCCLPFFLTSLCYLLIIRVLLKVEPESGLRV 240
QY 241 SHRKALTTIIITLIIFFLCFLPYHTLRVHLFTWKVGLCKDRILHKLVTTLALAAANACF 300
DB 241 SHRKALTTIIITLIIFFLCFLPYHTLRVHLFTWKVGLCKDRILHKLVTTLALAAANACF 300
QY 301 NPLLIYFAGEFNFRDKISALRKGPQKATKCVFPVSWLRKRETRY 346
DB 301 NPLLIYFAGEFNFRDKISALRKGPQKATKCVFPVSWLRKRETRY 346

RESULT 11
ABB05229

ID ABB05229 standard; protein; 346 AA.
XX ABB05229;
AC
XX 03-APR-2002 (first entry)
DT
XX Human LTD4-like G protein-coupled receptor protein SEQ ID NO.2.
DE
XX Human, LTD4-like G protein-coupled receptor; LTD4-like GPCR; antifungal;
KW antibacterial; antiviral; protozoacide; analgesic; cyostatic; cardiant;
KW hypotensive; hypertensive; antianginal; anorectic; anti-ulcer; nootropic;
KW antiallergic; antiallergic; antianginal; antiemetic; anticonvulsant;
KW immunostimulant; neuroprotective; neuroleptic; osteopathic; anti-HIV;
KW gene therapy; vaccine; infection; pain; cancer; diabetes; obesity;
KW anorexia; acute heart failure; hypotension; hypertension; osteoporosis;
KW angina pectoris; myocardial infarction; stroke; ulcer; asthma; allergy;
KW benign prostatic hypertrophy; migraine; vomiting; dementia; dyskinesia;
KW severe mental retardation; Huntington's disease; immunological response;
KW Gilles de la Tourette's syndrome.
XX
OS Homo sapiens.
XX
PN WO200194580-A1.
XX
XX 13-DEC-2001.
PD
XX 02-JUN-2001; 2001WO-BP006313.
PF
XX 06-JUN-2000; 2000EP-00112147.
PR
XX (MERB) MERCK PATENT GMBH.
XX
PA Kluxen F, Duecker K;
PI
XX WPI; 2002-130593/17.
DR
XX N-PSDB; ABA92899.
XX
PT New LTD4 receptor like G-protein coupled receptor polypeptide and
PT polynucleotide, useful in diagnostic assays and in identifying agonists
PT or antagonists for treating infections, pain, cancer, hypertension,
PT stroke, ulcers or asthma.
XX
PS Claim 1; Page 40; 43pp; English.
XX
CC The present sequence represents the human LTD4-like G protein-coupled
CC receptor (GPCR) protein (I). (I) and the polynucleotide (II) encoding it
CC have antifungal, antibacterial, antiviral, protozoacide, analgesic,
CC cyostatic, cardiant, hypotensive, hypertensive, antianginal, anorectic,
CC anti-ulcer, antiallergic, antiallergic, antianginal, antiemetic,
CC muscular, nootropic, anticonvulsant, immunostimulant, neuroprotective,
CC neuroleptic, osteopathic and anti-HIV activities, and can be used in gene
CC therapy and vaccine production. (I) and (II) can be used in diagnostic
CC assays. They can also be used in identifying compounds that may be
CC agonists or antagonists that are potentially useful in therapy, e.g. for
CC treating bacterial, fungal, protozoan or viral infections (e.g. HIV-1),
CC pain, cancers, diabetes, obesity, anorexia, acute heart failure,
CC hypertension, hypertension, osteoporosis, angina pectoris, myocardial
CC infarction, stroke, ulcers, asthma, allergies, benign prostatic
CC hypertrophy, migraine, vomiting, dementia, or severe mental retardation
CC or dyskinesias (e.g. Huntington's disease or Gilles de la Tourette's
CC syndrome). (I) and (II) can also be used in vaccines for inducing an
CC immunological response in a mammal
XX
SQ Sequence 346 AA:

Query Match 100.0%; Score 1788; DB 5; Length 346;
Best Local Similarity 100.0%; Pred. No. 2.7e-180;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MERKPMSTQPSISVSEMEPNGTFSNNRNCTIENFKRPFPIVYLIIFFMGVLNGLSI 60
DB 1 MERKPMSTQPSISVSEMEPNGTFSNNRNCTIENFKRPFPIVYLIIFFMGVLNGLSI 60

Db 241 SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKLAVITLALAAANCF 300
 QY 301 NPLLYFAGENFKDRKLSALRKGHPOKATKTCVFPVSVWLKRETRV 346
 Db 301 NPLLYFAGENFKDRKLSALRKGHPOKATKTCVFPVSVWLKRETRV 346

RESULT 13
 ABU11923
 ID ABU11923 standard; protein; 346 AA.
 AC ABU11923;
 XX
 DT 13-FEB-2003 (first entry)
 XX
 DE Human G-protein coupled receptor HGRPRMY11.
 XX
 KW Human; receptor; HGRPRMY11; HGRPRMY11v1; HGRPRMY11v2; GPCR74; GPCR81;
 KW G-protein coupled receptor; cardiovascular disease; arrhythmia;
 KW myocardial infarction; congestive heart failure; cardiomyopathy;
 KW atherosclerosis; arteriosclerosis; embolism; angina; thrombosis;
 KW hypertension; Alzheimer's disease; Parkinson's disease; osteoporosis;
 KW obesity; human immunodeficiency virus infection; HIV; schizophrenia;
 KW sleeplessness; acquired immunodeficiency syndrome; AIDS; leukemia;
 KW sepsis; inflammation; psoriasis; Gaucher's disease; ischaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200286123-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 16-NOV-2001; 2001WO-US044019.
 XX
 PR 17-NOV-2000; 2000US-0249613P.
 PR 21-DEC-2000; 2000US-0257611P.
 PR 16-JUL-2001; 2001US-0305818P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 PI Feder J, Nelson TC, Ramanathan C, Cacace AM, Barber LB;
 XX
 DR WPI; 2003-093137/08.
 DR N-PSDB; ABX56012.
 XX
 PT New human G-protein coupled receptor HGRPRMY11 polypeptide or
 PT polynucleotide, useful for preventing, treating or ameliorating e.g.
 PT myocardial infarction, angina, thrombosis, Alzheimer's disease,
 PT schizophrenia, AIDS, leukemia.
 XX
 PS Claim 33; Fig 6; 444pp; English.
 XX
 CC The invention relates to an isolated polypeptide (designated HGRPRMY11),
 CC which has a G-protein coupled receptor (GPCR) activity (also known as
 CC GPCR74 or GPCR81) and is encoded by the cDNA contained in ATCC Deposit
 CC Number PTA-2766, its variants (HGRPRMY11v1 and HGRPRMY11v2), fragments,
 CC domains, species homologues and proteins 95% similar to it. Also included
 CC are: (1) the nucleic acids encoding the HGRPRMY11 proteins (including
 CC variants, fragments, complements and sequences 95% similar to the
 CC HGRPRMY11 nucleic acids); (2) recombinant vectors; (3) transformed host
 CC cells expressing HGRPRMY11; (4) an anti-HGRPRMY11 antibody; (5)
 CC diagnosing a pathological condition or a susceptibility to a pathological
 CC condition in a subject; (6) identifying a binding partner to the
 CC HGRPRMY11 polypeptide; (7) identifying an activity in a biological assay;
 CC (8) a process for making polynucleotide sequences encoding a gene product
 CC having altered GPCR activity; (9) a shuffled polynucleotide produced by
 CC the method of (8); and (10) screening for candidate compounds capable of
 CC binding to and/or modulating activity of a GPCR. The polypeptide or the
 CC polynucleotide is useful for preventing, treating or ameliorating a
 CC medical condition, particularly cardiovascular diseases or disorders,
 CC e.g. myocardial infarction, congestive heart failure, arrhythmias,
 CC cardiomyopathy, atherosclerosis, arteriosclerosis, embolism, angina,
 CC thrombosis or hypertension). The HGRPRMY11 polypeptide or polynucleotide

CC is also useful for treating, preventing or ameliorating e.g. Alzheimer's
 CC disease, Parkinson's disease, osteoporosis, obesity, human
 CC immunodeficiency virus (HIV) infections, schizophrenia, sleeplessness,
 CC acquired immunodeficiency syndrome (AIDS), leukemia, sepsis,
 CC inflammations, psoriasis, Gaucher's disease or ischaemia (many other
 CC diseases and disorders are listed in the specification). The present
 CC sequence represents an HGRPRMY11 protein (or variant)
 XX

Seq Sequence 346 AA;
 Query Match 100.0%; Score 1789; DB 6; Length 346;
 Best Local Similarity 100.0%; Pred.No. 2.7e-180;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKFMSLQPSISVSEMEENGTFSSNNNSNCTIENPKRFPPIYVLIIFPWCVLNGLSI 60
 Db 1 MERKFMSLQPSISVSEMEENGTFSSNNNSNCTIENPKRFPPIYVLIIFPWCVLNGLSI 60
 QY 61 YVFLQPKKSTSVNFMLNLAIISDLIFSTLPFRADYYLRGSNMFGLDAGRIMSYSLYV 120
 Db 61 YVFLQPKKSTSVNFMLNLAIISDLIFSTLPFRADYYLRGSNMFGLDAGRIMSYSLYV 120
 QY 121 NMYSIYFLTVLSVVRFLAMVHPFLRLHVTSSIRSAWIIIGIIVILIMASSIMLDGSGSQ 180
 Db 121 NMYSIYFLTVLSVVRFLAMVHPFLRLHVTSSIRSAWIIIGIIVILIMASSIMLDGSGSQ 180
 QY 181 NSGVSQCLEMNYKAKIOTMNYIALVVGCLLPFTLSIYLLIRVLKXVPPSSGLRV 240
 Db 181 NSGVSQCLEMNYKAKIOTMNYIALVVGCLLPFTLSIYLLIRVLKXVPPSSGLRV 240
 QY 241 SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKLAVITLALAAANCF 300
 Db 241 SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRLHKLAVITLALAAANCF 300

QY 301 NPLLYFAGENFKDRKLSALRKGHPOKATKTCVFPVSVWLKRETRV 346
 Db 301 NPLLYFAGENFKDRKLSALRKGHPOKATKTCVFPVSVWLKRETRV 346

RESULT 14
 ABP81707
 ID ABP81707 standard; protein; 346 AA.
 AC ABP81707;
 XX
 DT 04-MAR-2003 (first entry)
 XX
 DE Human cysteinyl leukotriene CYS172 receptor protein SEQ ID NO:589.
 XX
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KW immunological-related cell proliferative disease; autoimmune disease;
 KW Alzheimer's disease; arteriosclerosis; infection; osteoarthritis; allergy;
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KW hypertension; hypotension; renal disorder; Rheumatoid arthritis; trauma;
 KW ulcer.
 XX
 OS Homo sapiens.
 XX
 PN WO200261087-A2.
 XX
 PD 08-AUG-2002.
 XX
 PF 19-DEC-2001; 2001WO-US050107.
 PF 19-DEC-2000; 2000US-0257144P.
 PR 19-DEC-2000; 2000US-0257144P.
 XX
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.
 XX

CC in raising specific antibodies that can block the receptor and
CC effectively prevent ligand binding. The invention is useful in gene
CC therapy. The present sequence is human cysteinyl leukotriene (CysLT2)-
CC like GPCR protein.
XX

Sequence 346 AA:

Query Match 100.0%; Score 1788; DB 7; Length 346;
Best Local Similarity 100.0%; Pred. No. 2.7e-180;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKFMSLQPSISVSEMEPNGTSSNNNSRNCCTIENFRREFPIVYLIIFFMGVLGNGLSI 60
DB 1 MERKFMSLQPSISVSEMEPNGTSSNNNSRNCCTIENFRREFPIVYLIIFFMGVLGNGLSI 60
QY 61 YVFLQPYKKSTSVNVFNLNLAISDLFI STLPRADYILRGSNWIFGDLACRIMSYSLYV 120
DB 61 YVFLQPYKKSTSVNVFNLNLAISDLFI STLPRADYILRGSNWIFGDLACRIMSYSLYV 120
QY 121 NMYSIYFLTVLSVVRFLAMVHPRLHVTIRSAMILGIIWILIMASSIMLLDSGSEQ 180
DB 121 NMYSIYFLTVLSVVRFLAMVHPRLHVTIRSAMILGIIWILIMASSIMLLDSGSEQ 180
QY 181 NGSVTSCLBLNLKYIAKLQTMNYIALVGGCLLPFTLSICYLLIIRVLLKVEVPESGLRV 240
DB 181 NGSVTSCLBLNLKYIAKLQTMNYIALVGGCLLPFTLSICYLLIIRVLLKVEVPESGLRV 240
QY 241 SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTWKVGCLCKDRLRKALVITLALAAANACF 300
DB 241 SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTWKVGCLCKDRLRKALVITLALAAANACF 300
QY 301 NPLLYYFAGENFKDRLKSAALRKGHPOKATKCVFPVSVMLRKETRV 346
DB 301 NPLLYYFAGENFKDRLKSAALRKGHPOKATKCVFPVSVMLRKETRV 346

Search completed: December 13, 2004, 17:49:19
Job time : 157 secs

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OM protein - protein search, using sw model

Run on: December 13, 2004, 17:35:53; Search time 189 Seconds

(without alignments)
1053.331 Million cell updates/sec

Title: US-09-980-049-1

Perfect score: 1788
Sequence: 1 MERKPMISLOPISVSEMEPN.....KATKCVFVSWLRKTRV 346

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: UniProt 02:*

1: uniprot_sprot:*

2: uniprot_tramb1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1788	100.0	346	1 CLT2_HUMAN	Q9N675 homo sapien
2	1788	100.0	346	2 AAH6160	AAH6160 homo sapi
3	1427.5	79.8	345	1 CLT2_PIG	Q95N03 sus scrofa
4	1204	67.3	309	2 Q8R528	Q8R528 mus muscu
5	1197	66.9	309	1 CLT2_MOUSE	Q92061 mus muscu
6	1187	66.4	309	1 CLT2_MOUSE	Q92459 rattus norv
7	567.5	31.7	339	1 CLT2_RAT	Q92468 rattus norv
8	563	31.5	340	1 CLT1_PIG	Q95N02 sus scrofa
9	560	31.3	352	1 CLT1_MOUSE	Q95J64 mus muscu
10	560	31.3	352	2 BAC28308	BAC28308 mus muscu
11	559	31.3	337	1 CLT1_HUMAN	Q9Y271 homo sapien
12	553	30.9	337	2 Q8IVT9	Q8IVT9 homo sapien
13	487.5	27.1	337	1 GP80_HUMAN	Q96P68 homo sapien
14	484.5	26.9	339	2 Q8N5S7	Q8N5S7 homo sapien
15	481.5	26.8	337	2 Q6Y1R5	Q6Y1R5 rattus norv
16	479	26.8	337	2 AAP32736	AAP32736 rattus no
17	477	26.7	347	2 Q7ZZA4	Q7ZZA4 brachydanio
18	473.5	26.5	349	2 O6P852	O6P852 xenopus tro
19	473.5	26.5	349	2 AAH61378	AAH61378 xenopus t
20	473.5	26.5	349	2 P2YR_MEIGA	P2YR_MEIGA gallus gall
21	470	26.3	362	1 P2YR_CHICK	P2YR_CHICK mus muscu
22	468	26.2	337	2 O6IYF8	O6IYF8 mus muscu
23	468	26.2	337	2 AAT10591	AAT10591 mus muscu
24	463.5	25.9	361	2 Q90X57	Q90X57 xenopus lae
25	459.5	25.7	339	2 O6N655	O6N655 mus muscu
26	459.5	25.7	339	2 AAH70439	AAH70439 mus muscu
27	457	25.6	357	2 Q9DE05	Q9DE05 raja erinac
28	456	25.5	249	2 AAR26537	AAR26537 chinchilla
29	456	25.5	249	2 AAR26537	AAR26537 chinchilla
30	454	25.4	373	1 P2YR_CAVPO	P2YR_CAVPO cavia porce
31	454	25.4	373	1 P2YR_CAVPO	P2YR_CAVPO cavia porce

ALIGNMENTS

RESULT 1	CLT2_HUMAN	STANDARD;	PRT;	346 AA.	Q7TMV7
AC	Q9N675; Q9HCO2;				Q9N677 mus muscu
DT	28-FEB-2003 (Rel. 41, Last sequence update)				Q92250 gallus gall
DT	05-JUL-2004 (Rel. 44, Last annotation update)				P49651 rattus norv
DE	Cysteiny1 leukotriene receptor 2 (CysLTR2) (P5EC0146) (HG57) (HPN321)				P47900 homo sapien
DE	(HGPCR21).				O6N655 homo sapien
GN	Name=CysLTR2; Synonyms=CysLTR2, CysLTR2R;				AAH61378 homo sapi
OS	Homo sapiens (Human).				P48042 Bos taurus
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				P49650 mus muscu
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				BAC28413 mus muscu
OX	NCBI_TaxID=9606;				BAC29506 mus muscu
RN	[1]				P32249 homo sapien
RP	SEQUENCE FROM N.A.				Q8N615 mus muscu
RC	TISSUE=Placenta;				
RX	MEDLINE=20374466; PubMed=10913337; DOI=10.1006/dbrc.2000.3140;				
RA	Takaaki J., Kamohara M., Matsumoto M., Saito T., Sugimoto T., Oca T.,				
RA	Nishikawa T., Kawai Y., Masuno Y., Isogai T., Suzuki Y., Sugano S.,				
RA	Furuchi K.;				
RT	"The molecular characterization and tissue distribution of the human				
RT	cysteiny1 leukotriene receptor 2 (CysLTR2) receptor.";				
RL	Biochem. Biophys. Res. Commun. 274:316-322(2000)				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20459128; PubMed=10851239; DOI=10.1074/jbc.M003490200;				
RA	Halse C.E., O'Dowd B.F., Figueroa D.J., Sawyer N., Nguyen T.,				
RA	Im D.-S., Stocco R., Bellefeuille J.N., Abramovitz M., Cheng R.,				
RA	Williams D.L., Jr., Zeng Z., Liu Q., Ma L., Clements M.K., Coulombe N.,				
RA	Liu Y., Austin C.P., George S.R., O'Neill G.P., Wetters K.M.,				
RA	Lynch K.R., Evans J.F.;				
RL	J. Biol. Chem. 275:30531-30536(2000)				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20545741; PubMed=11093801;				
RA	Nothacker H.-P., Wang Z., Zhu Y., Reinscheid R.K., Lin S.H.S.,				
RA	Civelli O.;				
RT	"Molecular cloning and characterization of a second human cysteiny1				
RT	leukotriene receptor: discovery of a subtype selective agonist.";				
RL	Mol. Pharmacol. 58:1607-1608(2000)				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=2040266; PubMed=12044878;				
RA	Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;				
RT	"Identification of G protein-coupled receptor genes from the human				
RT	genome sequence.";				
RL	FEBS Lett. 520:97-101(2002)				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RA	Kopatz S.A., Aronstam R.S., Sharma S.V.;				
RT	"cDNA clones of human proteins involved in signal transduction				
RT	sequenced by the Guthrie cDNA resource center (www.cdna.org).";				

6/2/02/2000

2/1/02/2000

Dec

RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 [6]
 RP SEQUENCE FROM N.A.
 RX PubMed=5057823; DOI=10.1038/nature02379;
 RA Dunham A., Matthews L.H., Burton J., Ashurst J.L., Howe K.L.,
 RA Ashcroft K.J., Beare D.M., Burford D.C., Hunt S.E.,
 RA Griffiths-Jones S., Jones M.C., Keenan S.J., Oliver K., Scott C.E.,
 RA Alincough R., Almeida J.P., Ambrose K.D., Andrews D.T.,
 RA Ahearn R.I.S., Babage A.K., Bagunley C.L., Bailey J., Banerjee R.,
 RA Barlow K.F., Bates K., Beasley H., Bird C.P., Bray-Allen S.,
 RA Brown A.J., Brown J.Y., Burrill W., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M.E., Clark S.Y., Clarke G., Clae C.M.,
 RA Chag S.C., Cobley V., Collins J.E., Corby N., Coville G.J.,
 RA Deloukas P., Dhami P., Dunham I., Dunn M., Barthow M.E.,
 RA Ellington A.G., Faulker L., Frankish A.G., Frankland J., French L.,
 RA Garner P., Garrett J., Gilbert U.G.R., Gibson C.J., Ghori J.,
 RA Grahm D.V., Griddle S.M., Griffiths C., Hall R.E., Hammond S.,
 RA Hartley J.L., Hart E.A., Heath P.D., Howden P.J., Huckle E.J.,
 RA Hunt P.J., Hunt A.R., Johnson C., Johnson D., Kay M., Kimberley A.M.,
 RA King A., Laird G.K., Langford C.J., Lawlor S., Leongamornlert D.A.,
 RA Lloyd D.M., Lloyd C., Loveland J.E., Lovell J., Martin S.,
 RA Mashegheh-Mohammadi M., McLaren S.J., McMurray A., Milne S.,
 RA Moore M.J.F., Nickerson B., Porter K.M., Rice C.M., Seale S.,
 RA Pelan S., Phillimore B., Porter K.M., Rice C.M., Seale S.,
 RA Sehara H.K., Showkhen R., Skuce C.D., Smith M., Steward C.A.,
 RA Sycamore N., Teeter J., Thomas D.W., Tracey A., Tromans A., Tubby B.,
 RA Wall M., Wallis J.M., West A.P., Whitehead S.L., Willey D.L.,
 RA Wilming L., Wray P.W., Wright M.W., Young L., Coulson A., Durbin R.,
 RA Hubbard T., Sulston J.E., Beck S., Bentley D.R., Rogers J., Ross M.T.,
 RT "The DNA sequence and analysis of human chromosome 13,"
 RL Nature 428:522-528(2004).
 [7]
 RP SEQUENCE OF 17-346 FROM N.A.
 RT Suga H.;
 RT Homo sapiens cysteinyl leukotriene receptor 1 like receptor.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
 mediated via a G-protein that activates a phosphatidylinositol-
 calcium second messenger system. Stimulation by BAY u9773, a
 partial agonist, induces specific contractions of pulmonary veins
 and might also have an indirect role in the relaxation of the
 pulmonary vascular endothelium. The rank order of affinities for
 the leukotrienes is LTC4 = LTD4 >> LTE4.
 CC SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Widely expressed, with highest levels in the
 heart, placenta, spleen, peripheral blood leukocytes and adrenal
 gland. In lung, expressed in the interstitial macrophages, and
 slightly in smooth muscle cells.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC -----
 DR EMBL, AB038269; BAB03601.1; -;
 DR EMBL, AF254664; AAG17281.1; -;
 DR EMBL, AF279611; AAK69485.1; -;
 DR EMBL, AB083603; BAB89316.1; -;
 DR EMBL, AY389504; AAO91330.1; -;
 DR EMBL, AL137118; CAC29102.1; -;
 DR EMBL, AB041644; BAB16379.1; -;
 DR Genew; HGNC:18274; CYSLTR2.
 DR MIM; 605666; -;
 DR GO; GO:0004974; F:leukotriene receptor activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR004071; CysLeuk_receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR01533; CYSLTR2CDPTR.

DR PRINTS; PR00237; GPCR_RHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; FALSE_NEG.
 DR PROSITE; PS02862; G_PROTEIN_RECPT_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 42
 FT TRANSMEM 43 63
 FT DOMAIN 64 72
 FT TRANSMEM 73 93
 FT DOMAIN 94 123
 FT TRANSMEM 124 144
 FT DOMAIN 145 154
 FT TRANSMEM 154 174
 FT DOMAIN 175 204
 FT TRANSMEM 205 225
 FT DOMAIN 226 245
 FT TRANSMEM 246 266
 FT DOMAIN 267 286
 FT TRANSMEM 287 307
 FT DOMAIN 308 346
 FT DISULFID 111 187
 FT CARBOHYD 20 20
 FT CARBOHYD 26 26
 FT CARBOHYD 30 30
 FT CARBOHYD 181 181
 SQ SEQUENCE 346 AA; 39635 MW; EBS44A42DDCESEB4 CRC64;
 Query Match 100.0%; Score 1788; DB 1; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1e-103;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MERKFMISLOPSISVSEMEBNGTFSSNNNSNCTENPKRFFPIVYLIIPFGVLANGLSI 60
 DB 1 MERKFMISLOPSISVSEMEBNGTFSSNNNSNCTENPKRFFPIVYLIIPFGVLANGLSI 60
 QY 61 YVFLQPKKSTSVNFMNLAIISDLFISTLPFRADYIRGSNWIFGDIACRIMSISLVY 120
 DB 61 YVFLQPKKSTSVNFMNLAIISDLFISTLPFRADYIRGSNWIFGDIACRIMSISLVY 120
 QY 121 NMYSTYPLTVSVRFLAMVHPRFLHWTISRSMIIICGIIWIIIMASSIMLLSGSSRO 180
 DB 121 NMYSTYPLTVSVRFLAMVHPRFLHWTISRSMIIICGIIWIIIMASSIMLLSGSSRO 180
 QY 181 NSGVSCTELNLYKIAKIQTMNYIALVVGCLIPFPLTISCYLLIIRVLKVEPESGLRV 240
 DB 181 NSGVSCTELNLYKIAKIQTMNYIALVVGCLIPFPLTISCYLLIIRVLKVEPESGLRV 240
 QY 241 SHRKALTTIIITIIIPFLCELPYHTLRVHLTTWKGCKDRILHVALVTTLAANACF 300
 DB 241 SHRKALTTIIITIIIPFLCELPYHTLRVHLTTWKGCKDRILHVALVTTLAANACF 300
 QY 301 NPLLYFAGENPKDKLSLRGHPKAKTKVFPVSWLRKRETV 346
 DB 301 NPLLYFAGENPKDKLSLRGHPKAKTKVFPVSWLRKRETV 346
 RESULT 2
 AAH69160
 ID AAH69160 PRELIMINARY; PRT; 346 AA.
 AC AAH69160;
 DT 10-MAY-2004 (TREMBLrel. 27, Created)
 DT 10-MAY-2004 (TREMBLrel. 27, Last sequence update)
 DT 10-MAY-2004 (TREMBLrel. 27, Last annotation update)
 DE Cysteinyl leukotriene receptor 2.
 GN CYSLTR2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Synthetic constructs;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapellato M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshlyak I., Caraminci P., Prange C.,
 RA Raba S.S., Loguolano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnarac P.H.,
 RA Richards S., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Vallalton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton B., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Blakeley A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RA Krzywnicki M.I., Skalek U., Smallus D.E., Schnerch A., Schein J.E.,
 RT "generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC TISUE-Synthetic constructs;
 RA Strauberg R.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC069160; AAI69160.1; -
 KW Receptor.
 SQ SEQUENCE 346 AA; 39635 MW; EB54A4A2DDC5EB4 CRC64;
 Query Match 100.0%; Score 1788; DB 2; Length 346;
 Best Local Similarity 100.0%; Pred. No. 1e-103;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RA Ohishi T., Soga T., Matsushima H., Furuchi K.;
 RT "Characterization of the cloned rat and porcine cysleinyl leukotriene
 RT receptor";
 RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Receptor for cysleinyl leukotrienes. The response is
 CC mediated via a G-protein that activates a phosphatidylinositol-
 CC calcium second messenger system (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 DR EMBL: AB052662; BAB60817.1; -
 DR InterPro: IPR004071; Cysleuk_Receptor.
 DR InterPro: IPR000276; GPCR_Rhodopn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS: PR01533; CYSTRRECPTR.
 DR PRINTS: PR00237; GPCRHOODOPN.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
 DR PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 43
 FT TRANSSEM 44 64
 FT DOMAIN 65 73
 FT TRANSSEM 74 94
 FT DOMAIN 95 124
 FT TRANSSEM 125 145
 FT DOMAIN 146 154
 FT TRANSSEM 155 175
 FT DOMAIN 176 205
 FT TRANSSEM 206 226
 FT DOMAIN 227 246
 FT TRANSSEM 247 267
 FT DOMAIN 268 287
 FT TRANSSEM 288 308
 FT DOMAIN 309 345
 FT DISUFID 112 188
 FT CARBOHYD 20 20
 FT CARBOHYD 29 29
 FT CARBOHYD 177 177
 FT CARBOHYD 184 184
 SQ SEQUENCE 345 AA; 39410 MW; 5D1B1F89BB95905 CRC64;
 Query Match 79.8%; Score 1427.5; DB 1; Length 345;
 Best Local Similarity 79.3%; Pred. No. 2.7e-81;
 Matches 275; Conservative 25; Mismatches 44; Indels 3; Gaps 2;

QY 300 FNNLLYYAGENFKDLKSLARKGHPQAKTKCVFVSVMLRKETRY 346
DB 301 FNNFLYYAGENFKDLKSLARKGRQ--KTRCGFSVCWLKKEITRY 345

RESULT 4
ID 08R528 PRELIMINARY; PRT; 309 AA.
AC 08R528;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DE 01-MAR-2004 (Tremblrel. 26, Last annotation update)
GN Cysteiny1 leukotriene 2 receptor.
OS Name=Cyslt2;
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22013942; PubMed=11854273;
RA Ogasawara H, Ishii S, Yokomizo T, Kakinuma T, Komine M,
RA Tamaki K, Shimizu T, Izumi T.
RT Characterization of Mouse Cysteiny1 Leukotriene Receptors mCysLT1 and
RT mCysLT2. DIFFERENTIAL PHARMACOLOGICAL PROPERTIES AND TISSUE
RT DISTRIBUTION.";
RL J. Biol. Chem. 277:18763-18768(2002).
DR EMBL; AB058930; BAB86881.1; -.
DR MGI; MGI:1917336; Cyslt2.
DR GO; GO:0016020; G-protein coupled receptor activity; IDA.
DR GO; GO:0001631; Fcysteiny1 leukotriene receptor activity; IDA.
DR InterPro; IPR004071; Cysleuk receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01533; CYSLTRREPTR.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS50262; G_PROTEIN_RECPR_F1_2; 1.
KW Receptor.
SQ SEQUENCE 309 AA; 35226 MW; 96FACC6B8A96974 CRC64;

Query Match 67.3%; Score 1204; DB 2; Length 309;
Best Local Similarity 73.4%; Pred. No. 2e-67;
Matches 226; Conservative 30; Mismatches 52; Indels 0; Gaps 0;
QY 17 MEPNGTFSSNNRNCTIENFKREPPPIVYLIFFGVINGNGISIVYFLQPYKKSSTVNVF 76
DB 1 MEVTGTFSSYSNRNCTIENFKREPPPIVYLIFFGVINGNGISIVYFLQCKKSSISVNVF 60
QY 77 MNLAISDDLFIISTLPFRADYLRGSNMIFGDLACRIMSYSYLVNMYSSIFLTVLSVVR 136
DB 61 MNLAISDDLFIISTLPFRADYLRGSNMIFGDLACRIMSYSYLVNMYSSIFLTVLSVVR 120
QY 137 FLAMHPPFLHNTSRSANILCGIITWILMSSIMLLSGSNGNSVTSCELANLYKXA 196
DB 121 FLATVHPFPMFHTSVRSAMILCGIITWILMSSIMLLSGSNGNSVTSCELANLYKXA 180
QY 197 KLOTMYIALVVGCLPFTFLISCYLLIRVLLKVEVPSGLRVSHRKALTTIITLIIF 256
DB 181 SLIIMHIAVAGFLPFLTLTTCYLLIRILKAEIPSGPRAARKKALTTIVIMNIF 240
QY 257 FLCFLPHTLRTVHLTTWKVGLCKDLHKAIVTTTLAAANACFNPFLYYFAGENFKDL 316
DB 241 LILCFLEPYHARLTLHVTWMDKSCGVLDHKAIVTTTLMAAANSCFNPFLYYFAGENFKAL 300
QY 317 KSLARKGH 324
DB 301 RALFSKVH 308

RESULT 5
ID CLT2_MOUSE
AC CLT2_MOUSE STANDARD; PRT; 309 AA.
QY 0920A1;

DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cysteiny1 leukotriene receptor 2 (CysLT2).
GN Name=Cyslt2; Synonyms=Cyslt2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=21601669; PubMed=11591709; DOI=10.1074/jbc.M107556200;
RA Hui Y, Yang G, Galczenski H, Figueroa D.J., Austin C.P.,
RA Copeland N.G., Gilbert D.J., Jenkins N.A., Funk C.D.,
RT "The murine cysteiny1 leukotriene 2 (CysLT2) receptor. cDNA and
RT genomic cloning, alternative splicing, and in vitro
RT characterization.";
RL J. Biol. Chem. 276:47489-47495(2001).
CC -1- FUNCTION: Receptor for cysteiny1 leukotrienes. The response is
CC mediated via a G-protein that activates a phosphatidylinositol-
CC calcium second messenger system. The rank order of affinities for
CC the leukotrienes is LTC4 = LTD4 >> LTE4.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Widely expressed at low levels, with highest
CC expression in the spleen, thymus and adrenal gland, and lower in
CC the kidney, brain and peripheral blood leukocytes.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC -----
DR EMBL; AF31658; MAK97354.1; -.
DR MGI; MGI:1917336; Cyslt2.
DR GO; GO:0016020; G-protein coupled receptor activity; IDA.
DR GO; GO:0001631; Fcysteiny1 leukotriene receptor activity; IDA.
DR InterPro; IPR004071; Cysleuk receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01533; CYSLTRREPTR.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS50237; G_PROTEIN_RECPR_F1_1; FALSE_NEG.
DR PROSITE; PS50262; G_PROTEIN_RECPR_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 26
FT TRANSMEM 27 47
FT DOMAIN 48 56
FT TRANSMEM 57 77
FT DOMAIN 78 98
FT TRANSMEM 99 119
FT DOMAIN 120 138
FT TRANSMEM 139 159
FT DOMAIN 160 187
FT TRANSMEM 188 208
FT DOMAIN 209 229
FT TRANSMEM 230 250
FT DOMAIN 251 271
FT TRANSMEM 272 292
FT DOMAIN 293 309
FT DISULFID 95 171
FT CARBOHYD 14 14
SQ SEQUENCE 309 AA; 35227 MW; 327B1A46EDD2A02 CRC64;

Query Match 66.9%; Score 1197; DB 1; Length 309;
Best Local Similarity 72.7%; Pred. No. 5.4e-67;
Matches 224; Conservative 31; Mismatches 53; Indels 0; Gaps 0;
QY 17 MEPNGTFSSNNRNCTIENFKREPPPIVYLIFFGVINGNGISIVYFLQPYKKSSTVNVF 76


```

Db 1 MEVGTGSSYSNRKCTIENFKREPPITYLLIFPMGALGNGFSIYVFLQTKKSTSVNVF 60
Qy 77 MLNLAISDLFIETLPFRADYYLRGSMNIFGDLACRIMSYSLYVMYSSITFLTVLSVVR 136
Db 61 MLNLAISDLFIETLPFRADYYLRGSMNIFGDLACRIMSYSLYVMYSSITFLTVLSVVR 120
Qy 137 FLAMVHPRLHTYSIRSAWILGIIWILMASSIMLDSGSEONGSTSCLELNLYKIA 196
Db 121 FOATVHPRMFHVSVRSAMWILGIIWVFMASLLVNVQSEKDNIIISCLELSPQKFK 180
Qy 197 KLQTMNYIALVVGCLLPFTLSICYLIIIRVLKVEPESGLRVSHRKALFTIITLIIIF 256
Db 181 SLIMNMHIAVAGFLPFLITVTCYLIIIRILKREIPESGPRAHRAKALTTIVIAMTIF 240
Qy 257 FLCELPYHTLRTHLTWKVGLCKDRHLKALVTTLAANAACFNPLLYPAGENPKDRL 316
Db 241 LICELPYHARTLTLVTDKDSQDVLHKAFTVITLMAANSCEFNPFLYPAGENPKARL 300
Qy 317 KSALRKQH 324
Db 301 RAIFSQKH 308

RESULT 6
CLUT2_RAT STANDARD; PRT; 309 AA.
AC 0924TG;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Cysteinyll leukotriene receptor 2 (CysLTR2) (RSPPTJ2).
GN Name=CysLTR2; Synonym=CysLT2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP Kamehara M., Takasaki J., Matsumoto M., Matsumoto S., Saito T.,
RA Ohishi T., Soga T., Matsushime H., Furuchi K.;
RT "Characterization of the cloned rat and porcine cysteinyl leukotriene
RT receptors.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
CC mediated via a G-protein that activates a phosphatidylinositol-
CC calcium second messenger system (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; AB052661; BAB0816.1; -.
DR RGD; 619797; CysLT2.
DR InterPro; IPR004071; Cysleuk_receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO1533; CYSLTRCPTR.
DR PROSITE; PS00237; GPCR_RHODOPSIN.
DR PROSITE; PS00262; G_PROTEIN_RECPT_P1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 26 Extracellular (Potential).
FT TRANSMEM 27 47 1 (Potential).
FT DOMAIN 48 56 Cytoplasmic (Potential).
FT TRANSMEM 57 77 2 (Potential).
FT DOMAIN 78 98 Extracellular (Potential).

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FT TRANSMEM 99 119 3 (Potential).
FT DOMAIN 120 137 Cytoplasmic (Potential).
FT TRANSMEM 138 158 4 (Potential).
FT DOMAIN 159 187 Extracellular (Potential).
FT TRANSMEM 188 208 5 (Potential).
FT DOMAIN 209 229 Cytoplasmic (Potential).
FT TRANSMEM 230 250 6 (Potential).
FT DOMAIN 251 271 Extracellular (Potential).
FT TRANSMEM 272 292 7 (Potential).
FT DOMAIN 293 309 Cytoplasmic (Potential).
FT DISULFID 95 171 By similarity.
FT CARBOHYD 14 14 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 156 166 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 167 167 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 309 AA; 35507 MW; A122AC8177879D56 CRC64;

Query Match 66.4%; Score 1187; DB 1; Length 309;
Best Local Similarity 73.1%; Pred. No. 2,3e-66;
Matches 225; Conservative 26; Mismatches 57; Indels 0; Gaps 0;

Qy 17 MEVGTGSSYSNRKCTIENFKREPPITYLLIFPMGALGNGFSIYVFLQTKKSTSVNVF 76
Db 1 MGVTGTPSYSDKRCCTIENFKRDFYPIYLLIFPMGALGNGFSIYVFLQTKKSTSVNVF 60
Qy 77 MLNLAISDLFIETLPFRADYYLRGSMNIFGDLACRIMSYSLYVMYSSITFLTVLSVVR 136
Db 61 MLNLAISDLFIETLPFRADYYLRGSMNIFGDLACRIMSYSLYVMYSSITFLTVLSVVR 120
Qy 137 FLAMVHPRLHTYSIRSAWILGIIWILMASSIMLDSGSEONGSTSCLELNLYKIA 196
Db 121 FLATAHFQWLHTSVRSAMWILGIIWVFMASGLLKRKGQKONNTTICFELNLQKFK 180
Qy 197 KLQTMNYIALVVGCLLPFTLSICYLIIIRVLKVEPESGLRVSHRKALFTIITLIIIF 256
Db 181 NLVNIANYIALVGVFLPFLITTCYLIIIRVLKVEIPESGPDAQKALTTIVIAMTIF 240
Qy 257 FLCELPYHTLRTHLTWKVGLCKDRHLKALVTTLAANAACFNPLLYPAGENPKDRL 316
Db 241 LICELPYHARTLTLVTDKDSQDVLHKAFTVITLMAANSCEFNPFLYPAGENPKARL 300
Qy 317 KSALRKQH 324
Db 301 RAIFSQKH 308

RESULT 7
CLUT1_RAT STANDARD; PRT; 339 AA.
AC 0924TG;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Cysteinyll leukotriene receptor 1 (CysLTR1).
GN Name=CysLTR1; Synonym=CysLT1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP Kamehara M., Takasaki J., Matsumoto M., Matsumoto S.,
RA Ohishi T., Soga T., Matsushime H., Furuchi K.;
RT "Characterization of cloned rat and porcine cysteinyl leukotriene
RT receptors.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for cysteinyl leukotrienes mediating
CC constriction of the microvascular smooth muscle during an
CC inflammatory response. This response is mediated via a G-protein
CC that activates a phosphatidylinositol-calcium second messenger
CC system (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----

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QY 144 FRLHWTISRSAMTLCGIWI-LIMASSIMLDSGSEONGSVTSCLEINLYKIAK--LQT 200
 Db 132 VQINILTHKKAKVCAIMFVLITSPFLMSTSYDEKKNNTCPPEPOXNOKHYLV 191
 QY 201 MNYIALVVGCLLPFTLSICYLILIRVLKVEPESGLRVSRRKATLTITITLIFLFCF 260
 Db 192 LHVSLVGVFIPIVILVICTMILITLTKNSMKN--ISRRKALIGIIVTAAFLISF 249
 QY 261 LPHYTLATVHLTTKRGVGLCD-----RLKALVITLALAAANACPNLLYFAGENF 312
 Db 250 MPYHIOHTIHLHF-----LHNDTKHCDVLRMOKSVXITLISLAASNCCEFDPLLYFSGGNF 305
 QY 313 KDRLSALRK 322
 Db 306 REGI-STFRK 314
 RESULT 9
 CLTI_MOUSE STANDARD; PRT; 352 AA.
 AC Q99JA4; Q9J071; Q9UK47;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cysteiny1 leukotriene receptor 1 (CysLTR1) (Cysteiny1 leukotriene D4 receptor) (LTD4 receptor)
 GN Name=CysLTR1; Synonyms=CysLTR, CysLTR;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STRAIN=129/SV;
 RX PubMed=1126226; DOI=10.1073/pnas.041624398;
 RA Maekawa A., Kanoka Y., Lam B.K., Austen K.F.;
 RT "Identification in mice of two isoforms of the cysteiny1 leukotriene 1
 RT receptor that result from alternative splicing."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12256-12261(2001).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6; TISSUE=Trachea;
 RX MEDLINE=1556333; PubMed=11705452; DOI=10.1016/S0006-2952(01)00774-2;
 RA Martin V., Sawyer N., Stocco R., Unett D., Letner M.R., Abramovitz M.,
 RA Funk C.D.;
 RT "Molecular cloning and functional characterization of murine
 RT cysteiny1-leukotriene 1 (CysLTR1) receptors."
 RL Biochem. Pharmacol. 62:1193-1200(2001).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Blood;
 RX MEDLINE=21240338; PubMed=11342226; DOI=10.1016/S0167-4781(00)00271-2;
 RA Mollerup J., Jorgensen S.T., Hougaard C., Hoffmann B.K.;
 RT "Identification of a murine cysteiny1 leukotriene receptor by
 RT expression in Xenopus laevis oocytes."
 RL Biochim. Biophys. Acta 1517:455-459(2001).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=T-cell;
 RA Ogasawara H., Izumi T., Shimizu T.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diacienko L., Maruska K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallian D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Folley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting R., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butcherfield Y.S.N., Krzywicki M.I., Skalska U., Smallue D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Receptor for cysteiny1 leukotrienes mediating
 CC constriction of the microvascular smooth muscle during an
 CC inflammatory response. This response is mediated via a G-protein
 CC that activates a phosphatidylinositol-calcium second messenger
 CC system. The rank order of affinities for the leukotrienes is LTD4
 CC >> LTE4 = LTC4 >> LTB4.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=Long;
 CC IsoId=Q99JA4-1; Sequence=Displayed;
 CC Name=2; Synonyms=Short;
 CC IsoId=Q99JA4-2; Sequence=VSP_001921;
 CC -1- TISSUE SPECIFICITY: Widely expressed, with higher expression in
 CC the lung and skin, intermediate levels in the heart, kidney and
 CC stomach and lower levels in several other tissues. Isoform 1 is
 CC the most abundant form in all tested tissues.
 CC -1- MISCELLANEOUS: MK-571, a selective antagonist, was shown to
 CC inhibit eosinophilia, bronchial hyperreactivity and microvascular
 CC leakage. Zafirlukast (Accolate) and pranlukast (Onon) were also
 CC shown to be selective antagonists.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF329272; AAK16715.1; -;
 DR EMBL; AF329272; AAK16716.1; -;
 DR EMBL; AF205830; AAK15433.1; -;
 DR EMBL; AF263370; AAF73047.1; -;
 DR EMBL; AB044087; BAA96809.1; -;
 DR EMBL; BC027102; AAK27102.1; -;
 DR HSSP; P34996; 1DDP.
 DR MGD; MGI:1926218; CysLTR1.
 DR GO; GO:0005887; C:integral to plasma membrane; IDA.
 DR GO; GO:0004974; F:leukotriene receptor activity; IDA.
 DR GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; IDA.
 DR InterPro; IPR004071; CysLeuk_receptor.
 DR InterPro; IPR000276; GPCR_KnoDpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR01533; CYSLTRRECPTR.
 DR PRINTS; PR00237; GPCRHHODPSN.
 DR PROSITE; PS00267; G_PROTEIN_RECP_F1; 1; FALSE_NGS.
 DR PROSITE; PS02652; G_PROTEIN_RECP_F1_2; 1.
 KW Alternative splicing; G-protein coupled receptor; Glycoprotein;
 KW Transmembrane.
 FT DOMAIN 1 43
 FT TRANSMEM 44 64
 FT DOMAIN 65 72
 FT TRANSMEM 73 93
 FT DOMAIN 94 121
 FT TRANSMEM 122 142
 FT DOMAIN 143 156
 FT TRANSMEM 157 177
 FT DOMAIN 178 208
 FT TRANSMEM 209 229
 FT 5 (Potential).
 FT Extracellular (Potential).
 FT Cytoplasmic (Potential).
 FT 2 (Potential).
 FT Extracellular (Potential).
 FT Extracellular (Potential).
 FT Cytoplasmic (Potential).
 FT 4 (Potential).
 FT Extracellular (Potential).
 FT 5 (Potential).

FT	DOMAIN	230	245	Cytoplasmic (Potential).
FT	TRANSMEM	246	266	6 (Potential).
FT	DOMAIN	267	291	Extracellular (Potential).
FT	TRANSMEM	292	312	7 (Potential).
FT	DOMAIN	313	352	Cytoplasmic (Potential).
FT	DISULFID	111	188	By similarity.
FT	CARBOHYD	15	15	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	19	19	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	26	26	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	184	184	N-linked (GlcNAc. . .) (Potential).
FT	VAMPPLIC	1	13	Missing (in isoform 2). /FTId=VSP_001921.
FT	CONFLICT	176	176	y -> d (in Ref. 3).
FT	SEQUENCE	352 AA,	40715 MM,	SDBC94B3F1CD0CAB CRC64;
SO	Query Match	31.3%;	Score 560;	DB 1; Length 352;
	Best Local Similarity	38.5%;	Pred. No. 2.6e-27;	
	Matches 117;	Conservative	69;	Mismatches 108; Indels 10; Gaps 6;
QY	26	NNSRCTIENFRKEEFPIVYLILFPMVGLNGLSIVYFLOPKKSTSVNVPMLNLAISDL	85	
DB	26	NNTCCHDITDERANQVSTMSVTSVSGFNGSFLVYLKITYHESAQAQVYMINALADL	85	
QY	86	LFISTLPRADYYLRGSNWITFGDLACRIMSSGLYNNMYSIVLTLSVREFLAWHFR	145	
DB	86	LCVCTLPRLRVVYVYHKKMKMLFGDFLCRLTLYVALYNLCSIFPMTAMSFRCVALIFPVQ	145	
QY	146	LLHVTISASMTLGGIWI-LIMASIMLLSGSQNSVNSCLEMLNLYIAK--LQTMN	202	
DB	146	NINLVTKKAPFCVLCGIWIFVLNLSPLTKSKSYDEKONTKCFPPONNOKKXVLLH	205	
QY	203	YIALVVGCLPFPFLISCYLLILIRVLKVEVPSGLRVSHRKALTTIIITLIFPLCFLP	262	
DB	206	YVSLFPGFIIFPVITIVCYTMILITLLKNTMKKN--MPSRRALGMIIVVAAFLVSPMP	263	
QY	263	YHTLRVTLTW--KVGICKD--RLHKLAVITLALAAANACPNLLYYPAGENFQDKS	318	
DB	264	YHIOHTLHLHLHSETRPCDSVLVRQKSVITLLSLAASNCDFPLLYPFGSGNFRRL-S	322	
QY	319	ALRK	322	
DB	323	TFRK	326	
RESULT 10	BAC28308	PRELIMINARY;	PRT;	352 AA.
ID	BAC28308			
AC	BAC28308;			
DT	14-APR-2004 (Tremblrel. 27, Created)			
DT	14-APR-2004 (Tremblrel. 27, Last sequence update)			
DT	14-APR-2004 (Tremblrel. 27, Last annotation update)			
DE	Adult male colon cDNA, RIKEN full-length enriched library,			
DE	clone:9030217A18 product:CYSTBRINYL LBUKOTRIENE 1 RECEPTOR LONG			
DE	ISOFORM, full insert sequence.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Buteljeostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Colon;			
RC	MEDLINE=22354683; PubMed=12466851;			
RA	The FANTOM Consortium,			
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;			
RA	"Analysis of the mouse transcriptome based on functional annotation of			
RT	60,770 full-length cDNAs."			
RT	Nature 420:563-573 (2002).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Colon;			
RC	MEDLINE=21085660; PubMed=11217851;			
RA	RIKEN FANTOM Consortium,			
RA	"Functional annotation of a full-length mouse cDNA collection."			

RL Nature 403:685-690 (2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=99279253; PubMed=10349636;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning."
 RL Meth. Enzymol. 303:19-44 (1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=20499374; PubMed=11042159;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 RT prepare full-length cDNA libraries for rapid discovery of new genes."
 RL Genome Res. 10:1617-1630 (2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Saaki N., Carninci P.,
 RA Kono H., Akiyama U., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
 RA Okazaki Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Kiyada Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RT sequencing pipeline with 384 multicapillary sequencer."
 RL Genome Res. 10:1757-1771 (2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno K., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiromoto K., Hiraoka T., Hirozane T.,
 RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kaizawa T.,
 RA Katoh H., Kawai Y., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohashi N., Okazaki Y.,
 RA Naito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Saeki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tagami A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK033476; BAC28308.1; -
 KW Receptor
 SQ SEQUENCE 352 AA; 40715 MW; 5BDC94B3F1CD0CAB CRC64;
 SQ
 Query Match 31.3%; Score 560; DB 2; Length 352;
 Best Local Similarity 38.5%; Pred. No. 2.6e-27;
 Matches 117; Conservative 69; Mismatches 108; Indels 10; Gaps 6
 Oy 26 NNSNCTENKREBEFFPIVYLLIFPVGVLNGSLSYIVLQPKKSTSVNFMNLIAISL 85
 Db 26 NNTGHDITDEFRNOYSTWISVISVYGFPGFSFVLYVLKTHESAAQCVMTINIALIDL 85
 Oy 86 LFISTLPRADYYLRGNSNMIGDLACRIMSYSLYNNYSSIVFTLVLSVEFLAMVHFR 145
 Db 86 LCVCTLPLRIVYVYVYHKKWFLGDFLCRTTYTALYVNLCSIFPMFMASFPCVALVPPVQ 145
 Oy 146 LIAHTYSIRSAMITLGIITW-LIMASSIMLDGSGFQNGSVTSCLEMLYKIAK--LQTMN 202
 Db 146 NINLVTOKRAFVCIIGIWIPIVILITSSPELMKYSYODEKNNTKCEPPONNOAKKVVILH 205
 Oy 203 YIALVWGCLPFFFTSLICSYLLIIRVLKVEVDESGLRVSHRKALTTITITLIIFLCFDP 262
 Db 206 YVSLPFGFIIPFVITIIYCYMTIILTLKNTMKKA--MSSRKAKIMITIVTPAFLVSPRP 263
 Oy 263 YHTLRVHLLTW--KVLGKCD-RILKALVITTLAAANACFNPILLYFAGENFKRLKS 318
 Db 264 YHIRTTHILHSHETPCDSVLVMQSKSVVITLISLANSCEPDFLYPFGSGNFRRRL-S 322

QY 319 ALRK 322
DB 323 TFRK 326

RESULT 11
CLT1_HUMAN STANDARD, PRT, 337 AA.
ID CLT1_HUMAN
AC Q9Y271
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cysteinyl leukotriene receptor 1 (CysLTR1) (Cysteinyl leukotriene D4 receptor) (LTD4 receptor) (HG55) (HMTF81).
GN Name=CysLTR1; Synonyms=CysLT1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX Lymph K.R., O'Neill G.P., Liu Q., Im D.-S., Sawyer N., Metters K.M., Colombe N., Abramovitz M., Figueroa D.J., Zeng Z., Connolly B.M., Bal C., Austen C.P., Chateaufort A., Stocco R., Greig G.M., Kargman S., Hooks S.B., Hosfield E., Williams D.L. Jr., Ford-Hutchinson A.W., Caskey C.T., Evans J.F.;
RT "Characterization of the human cysteinyl leukotriene CysLTR1 receptor.";
RL Nature 399:789-793(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte, peripheral blood monocytes, and spleen;
RX MEDLINE=99393629; PubMed=10462554;
RA Sarau H.M., Ames R.S., Chambers J., Ellis C., Elshoutbagy N., Herlihy N.C., Halsey W., Satche G., Muir A.T., Nuthalaganti P., Dykko G.M., Buckley P.T., Wilson S., Bergsma D.J., Hay D.W.P.;
RT "Identification, molecular cloning, expression, and characterization of a cysteinyl leukotriene receptor.";
RL Mol. Pharmacol. 56:657-663(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Warren C.N., Aronstam R.S., Sharma S.V.;
RT "cDNA clones of human proteins involved in signal transduction regulated by the G-protein coupled receptor (GPCR) family.";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for cysteinyl leukotrienes mediating bronchoconstriction of individuals with and without asthma. Stimulation by LTD4 results in the contraction and proliferation of smooth muscle, edema, eosinophil migration and damage to the mucus layer in the lung. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. The rank order of affinities for the leukotrienes is LTD4 > LTD4 = LTC4 > LTC4.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Widely expressed, with highest levels in spleen and peripheral blood leukocytes. Lower expression in several tissues, such as lung (mostly in smooth muscle bundles and alveolar macrophages), placenta, small intestine, pancreas, colon and heart.
CC -1- MISCELLANEOUS: Selective antagonists, such as montelukast (Singulair), zafirlukast (Accolate) and pranlukast (Onon), are used in the treatment of the asthma crisis.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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CC -----
DR EMBL; AF119711; AAD42285.1; -
DR EMBL; AF133266; AAD42778.1; -
DR EMBL; AY242130; AAO92297.1; -
DR HSSP; P34996; 1DD. CysLTR1.
DR Genem; HGNC:17451; CysLTR1.
DR MIM; 30201; -
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0005624; C: membrane fraction; TAS.
DR GO; GO:0004974; P: leukotriene receptor activity; TAS.
DR GO; GO:0007204; P: pyrolytic calcium ion concentration elevation; TAS.
DR GO; GO:0006952; P: defense response; TAS.
DR GO; GO:0007585; P: respiratory gaseous exchange; TAS.
DR InterPro; IPR004071; CysLeuk_receptor.
DR InterPro; IPR00276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR01533; CysLTR1.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; FALSE_NEG.
DR PROSITE; PS0262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Transmembrane.
FT DOMAIN 1 28
FT TRANSMEM 29 49
FT DOMAIN 50 57
FT TRANSMEM 58 78
FT DOMAIN 79 106
FT TRANSMEM 107 127
FT DOMAIN 128 141
FT TRANSMEM 142 162
FT DOMAIN 163 193
FT TRANSMEM 194 214
FT DOMAIN 215 230
FT TRANSMEM 231 251
FT DOMAIN 252 276
FT TRANSMEM 277 297
FT DOMAIN 298 337
FT DISULFID 96 173
FT CARBOHYD 6 6
FT CARBOHYD 169 169
FT CARBOHYD 180 180
FT CARBOHYD 262 262
SQ SEQUENCE 337 AA; 38541 MW; B9B53940F895F245 CRC64;
Query Match 31.3%; Score 559; DB 1; Length 337;
Best Local Similarity 38.0%; Pred. No. 2,9e-27;
Matches 116; Conservative 71; Mismatches 106; Indels 12; Gaps 7;
QY 27 NSRNC--TINPKRPPPIVYLIIFKGVGLNGLSIVFLQPKYKSTSVNFMNLAIISD 84
DB 10 SSATCHTIDDFRQNVSTYISWISVPGFNGFVLVLLTKYHKSAFOVMYINLAVAD 69
QY 85 LFLPSTLPFRADYVYLRGNSWIFGDLACRISYSGLVYMYSSIVFLTVLSVRFAMVHP 144
DB 70 LFLCVTLPLAVVYVYVHKGIWLPDFLCRSTVLYLVNLSIFPMFAMSFFRCIAVFPV 129
QY 145 RLHVTSIRSAWITLGGIWI-LIMASIMLDGSEONGSVTSCLEMLYKIAK--LQTM 201
DB 130 QNINLVQKARFVCGIWI-FVLTSSPFLMARPDQDKNNTCFEPDQONQKNHVLVL 189
QY 202 NYALVGVCLPPTTSICVLLIIRVLKVEVSGLRVSHRQALTYITTLIFPLCF 261
DB 190 HYSVLPVGFPIIPVIVICVTMIITLLKSKMKN--LSHKRAIGMIVVTAFAVLSFM 247
QY 262 PYHTLRVHVTW--KVGLCSD--RLHKALVITLAAANACNPILPYAGSNFKORLK 317
DB 248 PYHQTIRHPLHNETKPCDSVLRMOKSVVITLSLAASNCFDPLLYPSGGNFKRL- 306
QY 318 SALRK 322
DB 307 TFRK 311

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RESULT 12
O81V19 PRELIMINARY; PRT; 337 AA.
ID O81V19
AC O81V19;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Cysteiny1 leukotriene receptor 1.
GN Name-CYSTLR1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaeetz T.E.,
RA Brownstein M.J., Udell T.B., Toshyuk S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Feilley J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalka U., Smalins D.E., Schmech A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC035750; AAH35750.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004874; F:leukotriene receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.
DR InterPro; IPR004071; CysLeuk_receptor.
DR InterPro; IPR000276; GPCR_Rhodopn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PRO1533; CYSLRCPTR.
DR PRINTS; PRO0237; GPCRHDOPSN.
DR PROSITE; PSS0262; G_PROTEIN_RECPE_P1_2; 1.
KW Receptor.
SQ SEQUENCE 337 AA; 38485 MW; B9B09CE0FD305245 CRC64;

Query Match 30.9%; Score 553; DB 2; Length 337;
Best Local Similarity 37.7%; Pred. No. 6.8e-27;
Matches 115; Conservative 71; Mismatches 107; Indels 12; Gaps 7;
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OY 202 NYIALVVGCLPFPFTSLICYLILIRYLKVEYBESGLRVSHRKALTIITLILPFLCPL 261
DB 190 HVSLFVGFTIPFVIITVITLILTKSKSKKN--LSHKKAIQMIWVTAAPLVSTM 247
OY 262 PHTLTATVHTTW--KVGCLKD--RLHKAIVITLAAANACFNPLLYYPAGEFNFRUK 317
DB 248 PHTIGTITLHFLHNETKCDVSLFTWQSKSVITLSIAASCDFPLLYPFSGGNFRKL- 306
OY 318 SALRK 322
DB 307 STEFRK 311
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RESULT 13
ID GP80_HUMAN STANDARD; PRT; 337 AA.
AC O96P68; Q86TL1;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Probable G protein-coupled receptor GPR80 (P2Y-like nucleotide
DE receptor) (P2Y-like GPCR).
GN Name=GPR80; Synonyms=GPR39;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21458557; PubMed=11574155; DOI=10.1016/S0378-1119(01)00651-5;
RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vantl W.B., Arshlicko O.,
RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RT "Discovery and mapping of ten novel G protein-coupled receptor
RT genes.";
RL Gene 275:83-91(2001).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX PubMed=12098360;
RA Wittenberger T., Hellebrand S., Munck A., Kreienkamp H.-J.,
RA Schaller H.C., Hampe W.;
RT "GPR39, a new G protein-coupled receptor belonging to a new subgroup
RT of nucleotide receptors.";
RL BMC Genomics 3:17-17(2002).
[3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040266; PubMed=12044878;
RA Takeda S., Kadowaki S., Haga T., Takeasu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RT genome sequence.";
RL FEBS Lett. 520:97-101(2002).
[4]
RN [4]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
RA Teutsuni S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
[5]
RP SEQUENCE FROM N.A.
RC TISSUE=Thyroid;
RA Bruess M., Bonisch H., von Kugelgen I.;
RT "Molecular cloning and functional characterization of a new human p2y
RT receptor";
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Orphan receptor.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Detected in kidney and, to a lower extend, in
CC placenta. Not detected in brain tissues including the frontal
CC cortex, caudate putamen, thalamus, hypothalamus, hippocampus or
CC pons.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
```

RESULT 14	GP17_HUMAN	STANDARD;	PRT; 367 AA.
ID	GP17_HUMAN	STANDARD;	PRT; 367 AA.
AC	Q13304;Q9UD26; Q9UB21.		
DT	01-NOV-1997 (Rel. 35, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Probable P2Y purinoceptor GPR17 (P2Y-1like receptor) (R12).		
GN	Name=GPRI7;		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A. (ISOFORM 2).		
RX	MEDLINE=96145150; PubMed=8558062;		
RA	Report C.J., Schweickart V.L., Chantry D., Eddy R.L. Jr., Shows T.B.,		
RA	Godista R., Gray P.W.;		
RT	"New members of the chemokine receptor gene family.";		
RL	J. Leukoc. Biol. 59:18-23(1996).		
CC	[2]		
CC	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).		
CC	TISSUE=Hippocampus;		
RX	MEDLINE=98181695; PubMed=9523551;		
RA	Blaesius R.H., Weber R.G., Licher P., Ogilvie A.;		
RT	"A novel orphan G protein-coupled receptor primarily expressed in the		
RT	brain is localized on human chromosomal band 2q21.";		
RL	J. Neurochem. 70:1357-1365(1998).		
CC	-1- PUNCTON: Putative receptor for putines coupled to G-proteins (By		
CC	similarity).		
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.		
CC	-1- ALTERNATIVE PRODUCTS:		
CC	Event=Alternative splicing; Named isoforms=2;		
CC	Name=1;		
CC	Isoid=Q13304-1; Sequence=Displayed;		
CC	Name=2;		
CC	Isoid=Q13304-2; Sequence=VSP_001987;		
CC	-1- TISSUE SPECIFICITY: Primarily expressed in brain.		
CC	-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.		
CC	-----		
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CC	or send an email to license@sib-sib.ch).		
CC	-----		
DR	EMBL; U33447; AAB16746.1; -		
DR	EMBL; Y12546; CA73144.1; -		
DR	EMBL; Z94154; CAB08107.1; -		
DR	EMBL; Z94155; CAB08108.1; -		
DR	HSSP; P34596; 1DDO.		
DR	Genew; HGNC:4471; GPR17.		
DR	MIT; 603071; -		
DR	GO; GO:0003867; C:integral to plasma membrane; TAS.		
DR	GO; GO:0004350; F:chemokine receptor activity; TAS.		
DR	GO; GO:0007186; P:G-protein coupled receptor protein signaln. ; TAS.		
DR	InterPro; IPRO00276; GPCR Rhodops.		
DR	InterPro; IPRO02286; P2_purinoceptor.		
DR	Pfam; PPF00001; 7tm.1; 1		
DR	PRINTS; PR00237; GPCRKHODPSN.		
DR	PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.		
DR	PROSITE; PS50263; G_PROTEIN_RECP_F2_1; 1.		
KW	Alternative splicing; G-protein coupled receptor; Glycoprotein;		
KW	Transmembrane.		
FT	DOMAIN 1 64		Extracellular (Potential).
FT	TRANSEM 65 85		1 (Potential)
FT	DOMAIN 86 92		Cytoplasmic (Potential).
FT	TRANSEM 93 113		2 (Potential)
FT	DOMAIN 114 133		Extracellular (Potential).

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FT TRANSMEM 134 154 3 (Potential).
FT DOMAIN 155 175 Cytoplasmic (Potential).
FT TRANSMEM 176 196 4 (Potential).
FT DOMAIN 197 223 Extracellular (Potential).
FT TRANSMEM 224 244 5 (Potential).
FT TRANSMEM 245 260 Cytoplasmic (Potential).
FT TRANSMEM 261 281 6 (Potential).
FT DOMAIN 282 308 Extracellular (Potential).
FT TRANSMEM 309 329 7 (Potential).
FT DOMAIN 330 367 Cytoplasmic (Potential).
FT DISULFID 132 209 By similarity.
FT CARBOHYD 42 42 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 204 204 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 282 282 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 1 28 Missing (in isoform 2).
SQ SEQUENCE 367 AA; 40989 MW; 132PBE97BE83C60C CRC64;

Query Match 27.1%; Score 484.5; DB 1; Length 367;
Best Local Similarity 34.4%; Pred. No. 1.3e-22;
Matches 116; Conservative 65; Mismatches 131; Indels 25; Gaps 10;

QY 11 SISVSEMPNG--TFSNNNSRNTIEN-FKREFFPIVYIIFFWGLGNGLSIYVFLQIP 66
DB 28 SNNGLVAPPGGLITNFSIATAEQCGQETPLENMLFASFYLDFTLALVGNLTALMLFIRD 87
QY 67 YKKSSTVNVPMNLAIISDLFIETLPFRADYLRGSGNWIFGDLACRIMSYLVNMYSS 126
DB 88 HKSSTPANNVPMNLAAVADLSCLVLPRLVYHPSGNHWPGEIACLTGLFYLMNYASI 147
QY 127 YFTLVSVVFLAMVHFRLLHTYSIRSAMIIGIWIIL-MASSIMLDSGSEONGSVT 185
DB 148 YFTICISADRFIAIVHVSCLKRRPLVYAHLCAPFLVAVVAVMAPLVSPQVQTHVY 207
QY 186 SCLEMLYKIAKIQTMNYIALVVGCLPFFTLISCYLLIRVLAKVEPSGLRVSHR-- 243
DB 208 VCLQ--LYR-EKASHHALVSLAVAFTEPFIITVTCYLLIIRSL-----RQGLRVEKRLK 258
QY 244 -KALTIIITLIFLFCFLPYHLLRTVHLTWKV--GLCKDRLHKLV--ITLALANNA 298
DB 259 TKAVRMALVLAFLVCFVPHVNRSVYVLYHSHGASCATQRIILANRITSLTSLNG 318
QY 299 CFNPDLFFAGENFKDLKSAI-----RKGHPOKAKTK 331
DB 319 ALDPIMYFVAEKFRHALLCNLLCGKRLKGPSPPEBK 355

RESULT 15
Q8NS57 PRELIMINARY; PRT; 339 AA.
AC Q8NS57;
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE GPR17 protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Rahay U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Skimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.J., Gilmour U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RA Strausberg R.;
EMBL; BC031653; AAH31653.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity; G-. . . IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . IEA.
DR InterPro; IPR002766; GPCR_Rhodopsn.
DR InterPro; IPR002286; P2_purinocptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PRINTS; PR01157; P2PURNOCPTR.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
SQ SEQUENCE 339 AA; 37860 MW; BB0CAF0FC371D63 CRC64;

Query Match 26.9%; Score 481.5; DB 2; Length 339;
Best Local Similarity 34.6%; Pred. No. 1.9e-22;
Matches 115; Conservative 62; Mismatches 130; Indels 25; Gaps 10;

QY 16 EMEPNG--TFSNNNSRNTIEN-FKREFFPIVYIIFFWGLGNGLSIYVFLQIPYKST 71
DB 5 EVAPPGGLITNFSIATAEQCGQETPLENMLFASFYLDFTLALVGNLTALMLFIRHKSQT 64
QY 72 SYNVMNLNLAISDLFIETLPFRADYLRGSGNWIFGDLACRIMSYLVNMYSSITV 131
DB 65 PANNVPMNLAAVADLSCLVLPRLVYHPSGNHWPGEIACLTGLFYLMNYASIYFLIC 124
QY 133 LSVVFLAMVHFRLLHTYSIRSAMIIGIWIIL-MASSIMLDSGSEONGSVTSCLEL 190
DB 125 ISADRFIAIVHVSCLKRRPLVYAHLCAPFLVAVVAVMAPLVSPQVQTHVYVCLQ 183
QY 191 NIYIAKIQTMNYIALVVGCLPFFTLISCYLLIRVLAKVEPSGLRVSHR--KALT 247
DB 184 -LYR-EKASHHALVSLAVAFTEPFIITVTCYLLIIRSL-----RQGLRVEKRLKTKAVR 235
QY 248 TIIITLIFLFCFLPYHLLRTVHLTWKV--GLCKDRLHKLV--ITLALANNA 303
DB 236 MIAIVLAFLVCFVPHVNRSVYVLYHSHGASCATQRIILANRITSLTSLNGALDPI 295
QY 304 LYPFAGENFKDLKSAI-----RKGHPOKAKTK 331
DB 296 MYFVAEKFRHALLCNLLCGKRLKGPSPPEBK 327

Search completed: December 13, 2004, 17:52:34
Job time : 191 secs

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OM protein - protein search, using sw model

Run on: December 13, 2004, 17:44:09 ; Search time 40 Seconds
(Without alignments)
573.651 Million cell updates/sec

Title: US-09-980-049-1

Perfect score: 1788
Sequence: 1 MERKMSLOPISVSSEMEPN.....KATKCVFVSWLRKRETV 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/prodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/prodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/prodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/prodata/1/1aa/PC/US.COMB.pep.*
6: /cgn2_6/prodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1779	99.5	346	US-09-585-876-2	Sequence 2, App1
2	559	31.3	337	US-09-044-404A-2	Sequence 2, App1
3	559	31.3	337	US-09-586-924-2	Sequence 2, App1
4	483.5	27.0	339	US-08-153-848-44	Sequence 4, App1
5	483.5	27.0	339	US-08-812-871-3	Sequence 3, App1
6	483.5	27.0	339	US-09-299-843A-44	Sequence 4, App1
7	483.5	27.0	339	US-09-088-337B-44	Sequence 4, App1
8	483.5	27.0	339	US-09-170-496D-32	Sequence 3, App1
9	483.5	27.0	339	PCT-US93-11153-44	Sequence 4, App1
10	483.5	27.0	339	PCT-US95-07180-2	Sequence 2, App1
11	480.5	26.9	339	US-09-170-496D-182	Sequence 182, App
12	464	25.0	362	US-08-513-974B-374	Sequence 2, App1
13	447.5	25.0	370	US-08-781-250-2	Sequence 3, App1
14	446	24.9	373	US-09-745-842-14	Sequence 14, App1
15	442	24.7	373	US-08-559-524A-4	Sequence 4, App1
16	442	24.7	373	US-08-749-707-4	Sequence 4, App1
17	442	24.7	373	US-09-947-922-4	Sequence 4, App1
18	440	24.6	361	US-08-383-750-4	Sequence 4, App1
19	440	24.6	361	US-08-352-678-4	Sequence 4, App1
20	440	24.6	361	US-09-536-954-4	Sequence 4, App1
21	440	24.6	361	US-09-170-496D-78	Sequence 78, App1
22	440	24.6	361	US-09-929-583B-4	Sequence 4, App1
23	440	24.6	361	PCT-US93-09636-4	Sequence 4, App1
24	439.5	24.6	348	US-08-852-824-17	Sequence 17, App1
25	439	24.6	302	US-08-467-948A-30	Sequence 30, App1
26	439	24.6	302	US-08-467-947A-30	Sequence 30, App1
27	437	24.4	344	US-08-467-948A-8	Sequence 8, App1

ALIGNMENTS

28	437	24.4	344	3	US-08-467-947A-8	Sequence 8, App1
29	434	24.3	361	4	US-09-170-496D-206	Sequence 206, App
30	434	24.3	377	4	US-09-745-842-17	Sequence 17, App1
31	424.5	23.7	374	4	US-09-745-842-15	Sequence 15, App1
32	419.5	23.5	373	3	US-08-513-974B-373	Sequence 373, App
33	419.5	23.5	374	4	US-09-102-710B-3	Sequence 3, App1
34	416	23.3	342	3	US-08-988-876-9	Sequence 9, App1
35	416	23.3	375	1	US-08-442-134A-2	Sequence 2, App1
36	416	23.3	375	1	US-08-444-581B-2	Sequence 2, App1
37	416	23.3	375	1	US-08-446-088A-2	Sequence 2, App1
38	416	23.3	375	2	US-08-559-524A-3	Sequence 3, App1
39	416	23.3	375	3	US-08-749-707-3	Sequence 3, App1
40	416	23.3	375	4	US-09-947-922-3	Sequence 3, App1
41	409.5	22.9	342	4	US-09-054-272-2	Sequence 2, App1
42	406.5	22.7	398	1	US-08-097-938-6	Sequence 6, App1
43	406.5	22.7	398	1	US-08-476-000-6	Sequence 6, App1
44	406.5	22.7	398	1	US-08-472-840-6	Sequence 6, App1
45	406.5	22.7	398	2	US-08-476-976-6	Sequence 6, App1

RESULT 1

US-09-585-876-2
; Sequence 2, Application US/09585876
; Patent No. 6586205
; GENERAL INFORMATION:
; APPLICANT: Gluckemann, Maria Alexandra
; TITLE OF INVENTION: 43239, A No. 6586205el GPCR-Like Molecule and
; FILE REFERENCE: 5800-88
; CURRENT APPLICATION NUMBER: US/09/585,876
; CURRENT FILING DATE: 2000-06-01
; EARLIER APPLICATION NUMBER: 60/182,061
; EARLIER FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-585-876-2

Query Match 99.5%; Score 1779; DB 4; Length 346;
Best Local Similarity 99.4%; Pred. No. 3.7e-131;
Matches 344; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	MERKMSLOPISVSSEMEPNGTSSNNRRTTBNKRREFFPIVYLIIFFWGLGNGLSI	60
DB	1	MERKMSLOPISVSSEMEPNGTSSNNRRTTBNKRREFFPIVYLIIFFWGLGNGLSI	60
QY	61	YVFLQYKSTSTNVNMLALSDLFISTLPRAADYVYRGSNWIMGDLACRIMSYSLVY	120
DB	61	YVFLQYKSTSTNVNMLALSDLFISTLPRAADYVYRGSNWIMGDLACRIMSYSLVY	120
QY	121	NMTSYIFLVLSVVFPLAMVHPFRLIHTYSIRSAWILGIIWILIMASSIMLDGSGSQ	180
DB	121	NMTSYIFLVLSVVFPLAMVHPFRLIHTYSIRSAWILGIIWILIMASSIMLDGSGSQ	180
QY	181	NGSVTSCLEINLYKINKQTMNTIALVVGCLPFFTLSTCYLLIIVLAKVEPESGLRV	240
DB	181	NGSVTSCLEINLYKINKQTMNTIALVVGCLPFFTLSTCYLLIIVLAKVEPESGLRV	240
QY	241	SHRKATTTTTIITIFFLCFLPYHTLRTVHLTWKVGCLCDRLAKALVTTLAANACP	300
DB	241	SHRKATTTTTIITIFFLCFLPYHTLRTVHLTWKVGCLCDRLAKALVTTLAANACP	300
QY	301	NPLLYVFAGENFDRKLSALRKQHPQAKTKCVFVSWLRKRETV	346
DB	301	NPLLYVFAGENFDRKLSALRKQHPQAKTKCVFVSWLRKRETV	346

RESULT 2

```

US-09-044-404A-2
; Sequence 2, Application US/09044404A
; Patent No. 6200775
; GENERAL INFORMATION:
; APPLICANT: SATHI, GANESH
; APPLICANT: HALSEY, WENDY
; APPLICANT: ELIS, CATHERINE
; APPLICANT: AMES, ROBERT
; APPLICANT: FOLEY, JAMES
; APPLICANT: SARAU, HENRY
; TITLE OF INVENTION: CDNA CLONE HMTMF81 THAT ENCODES
; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 790 Swedeland Road, P.O. Box 1539
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,404A
; FILING DATE: MARCH 19, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/844,795
; FILING DATE: APRIL 22, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T.
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: GH-70001-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 337 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-044-404A-2

```

Query Match 31.3%; Score 559; DB 3; Length 337;

Best Local Similarity 38.0%; Pred. No. 3.6e-36; Matches 116; Conservative 71; Mismatches 106; Indels 12; Gaps 7;

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27 NSRNC--TIENFKREFFPIVYIIIFWGLANGLSIYFLOPKYKSTSVNFMMLAISD 84
10 SSATCHDITDDPRNQVSTLYSMISVGFNGFVLYVLIKTHKSAQVVMINLAVD 69
85 ILFISTLPFRADYYLRGSMWIFGDLACRIMSYSLVNMYSIYFVLTVLSVRFAMWHP 144
70 LNCVCTLPRLVVYVYHKGIMLFGDFLCRLSTYALVNLCSIFPMTAMSPFCIALVFPV 129
145 RLHVTISRSAMIIGIIMI-LIMASSIMLDSGSEONGSVTSCLEMLYKIAK--LQTM 201
130 QNINLVTKKARFVCGVIMIPVILTSPPFLMAKPKQDKGNNTKCFPPQDNOTKNHVL 189
202 NYIALVVGCLPFTLSICYLIIRVLLKVEVPESGLRVSHRKALTTIITLIIFFLCFL 261
190 HYVSLFVGFIIPVILVYVYHKGIMLFGDFLCRLSTYALVNLCSIFPMTAMSPFCIALV 247
262 PYHTLRTVHLTTW--KVGLCD--RLHKAIVTTLAALANACFNPLLYYPAGEFNRKRL 317

```

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Db 248 PYHIOHTIHLPHNETKPCDSVLMQKSVITLTLAASNCDFDLVYFSGGNFRKRL- 306
Qy 318 SALRK 322
Db 307 STFRK 311

```

RESULT 3

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US-09-586-924-2
; Sequence 2, Application US/09586924
; Patent No. 6506878
; GENERAL INFORMATION:
; APPLICANT: SATHI, GANESH M.
; APPLICANT: HALSEY, WENDY
; APPLICANT: ELIS, CATHERINE E.
; APPLICANT: AMES, ROBERT S.
; APPLICANT: FOLEY, JAMES J.
; APPLICANT: SARAU, HENRY M.
; APPLICANT: CHAMBERS, JON
; TITLE OF INVENTION: CDNA CLONE HMTMF81 THAT ENCODES A NOVEL
; TITLE OF INVENTION: HUMAN 7-TRANSMEMBRANE RECEPTOR
; FILE REFERENCE: GH-70001-1D1
; CURRENT APPLICATION NUMBER: US/09/586,924
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 09/044,404
; PRIOR FILING DATE: 1998-03-19
; PRIOR APPLICATION NUMBER: 08/844,795
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 2
; LENGTH: 337
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-586-924-2

```

Query Match 31.3%; Score 559; DB 4; Length 337;

Best Local Similarity 38.0%; Pred. No. 3.6e-36; Matches 116; Conservative 71; Mismatches 106; Indels 12; Gaps 7;

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27 NSRNC--TIENFKREFFPIVYIIIFWGLANGLSIYFLOPKYKSTSVNFMMLAISD 84
10 SSATCHDITDDPRNQVSTLYSMISVGFNGFVLYVLIKTHKSAQVVMINLAVD 69
85 ILFISTLPFRADYYLRGSMWIFGDLACRIMSYSLVNMYSIYFVLTVLSVRFAMWHP 144
70 LNCVCTLPRLVVYVYHKGIMLFGDFLCRLSTYALVNLCSIFPMTAMSPFCIALVFPV 129
145 RLHVTISRSAMIIGIIMI-LIMASSIMLDSGSEONGSVTSCLEMLYKIAK--LQTM 201
130 QNINLVTKKARFVCGVIMIPVILTSPPFLMAKPKQDKGNNTKCFPPQDNOTKNHVL 189
202 NYIALVVGCLPFTLSICYLIIRVLLKVEVPESGLRVSHRKALTTIITLIIFFLCFL 261
190 HYVSLFVGFIIPVILVYVYHKGIMLFGDFLCRLSTYALVNLCSIFPMTAMSPFCIALV 247
262 PYHTLRTVHLTTW--KVGLCD--RLHKAIVTTLAALANACFNPLLYYPAGEFNRKRL 317
248 PYHIOHTIHLPHNETKPCDSVLMQKSVITLTLAASNCDFDLVYFSGGNFRKRL- 306
Qy 318 SALRK 322
Db 307 STFRK 311

```

RESULT 4

```

US-08-153-848-44
; Sequence 44, Application US/08153848
; Patent No. 5759804
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schweikart, Vicki L.

```

```

; TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; City: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/153,848
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5759804and, Grete B.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-08-153-848-44

```

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Query Match      27.0%; Score 483.5; DB 1; Length 339;
Best Local Similarity 34.6%; Pred. No. 2.7e-30;
Matches 115; Conservative 63; Mismatches 129; Indels 25; Gaps 10;

```

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QY 16 EMBPNG--TFSSNNNSNCTIEN-FKREPPYVLIIFPMGVANGSIYFLOPYKST 71
DB 5 EVAPPGIITFSLATBACQCEETPLENMLPASFYLDFFIALVGNLTALMLFIRDKSGT 64
QY 72 SVNVFMLNTAISDLFLSTLPFRADYYLRGSNMIFGDLACRINSYSLYNNMYSIYFLTV 131
DB 65 PAVVFLMHLAVADLSCLVLPTRLYVHFGSNHMPFGELACRLTGFLYLMVYSIYFLTC 124
QY 132 LSVVRFLAMVHPPRLHVTISIRSAMILCGIIMILI-MASSIMLLDGSSENGSVTSCLEL 190
DB 125 ISADRFALIVHPVKSILRRPLVAMHLACAFLMVVAVAMAPLVSPTVQTNHTVCLQ- 183
QY 191 NLKIAKLQTMNTALVAVGCLPFTLSICYLIIIRVLKVEVBSGLRVSHR---KALT 247
DB 184 -LVR-EKASHRALVSLAVAFPTPTTVTCYLIILISL-----RQGLRVEKRLKTKAVR 235
QY 248 TIIITLIIIFLCPLPYHTLRTVHLTWKV--GLCKDLHKLAV--ITLALAAANACFNPL 303
DB 236 MIAIVLAIFVCPVPHVNRSVYVLAHRSHGASCATORIALANRITSCLSINGALDPI 295
QY 304 LYYFAGENFKDRLSAL---RKGHPOKAKTK 331
DB 296 MYFVAEKFRHALCNLLCGKRLKQPPSPFGK 327

```

```

RESULT 5
US-08-812-871-3
; Sequence 3, Application US/08812871
; Patent No. 5955303
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice

```

```

; APPLICANT: Guegler, Karl
; APPLICANT: Muzong Cheng
; TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; City: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,871
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0237 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: Genbank
; CLONE: 992700
;
US-08-812-871-3

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Query Match      27.0%; Score 483.5; DB 2; Length 339;
Best Local Similarity 34.6%; Pred. No. 2.7e-30;
Matches 115; Conservative 63; Mismatches 129; Indels 25; Gaps 10;

```

```

QY 16 EMBPNG--TFSSNNNSNCTIEN-FKREPPYVLIIFPMGVANGSIYFLOPYKST 71
DB 5 EVAPPGIITFSLATBACQCEETPLENMLPASFYLDFFIALVGNLTALMLFIRDKSGT 64
QY 72 SVNVFMLNTAISDLFLSTLPFRADYYLRGSNMIFGDLACRINSYSLYNNMYSIYFLTV 131
DB 65 PAVVFLMHLAVADLSCLVLPTRLYVHFGSNHMPFGELACRLTGFLYLMVYSIYFLTC 124
QY 132 LSVVRFLAMVHPPRLHVTISIRSAMILCGIIMILI-MASSIMLLDGSSENGSVTSCLEL 190
DB 125 ISADRFALIVHPVKSILRRPLVAMHLACAFLMVVAVAMAPLVSPTVQTNHTVCLQ- 183
QY 191 NLKIAKLQTMNTALVAVGCLPFTLSICYLIIIRVLKVEVBSGLRVSHR---KALT 247
DB 184 -LVR-EKASHRALVSLAVAFPTPTTVTCYLIILISL-----RQGLRVEKRLKTKAVR 235
QY 248 TIIITLIIIFLCPLPYHTLRTVHLTWKV--GLCKDLHKLAV--ITLALAAANACFNPL 303
DB 236 MIAIVLAIFVCPVPHVNRSVYVLAHRSHGASCATORIALANRITSCLSINGALDPI 295
QY 304 LYYFAGENFKDRLSAL---RKGHPOKAKTK 331
DB 296 MYFVAEKFRHALCNLLCGKRLKQPPSPFGK 327

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RESULT 6
US-09-299-843A-44

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/ Sequence 44, Application us/09299843A
/ Patent No. 6107475
/ GENERAL INFORMATION:
/ APPLICANT: Godiska, Ronald
/ APPLICANT: Gray, Patrick W.
/ APPLICANT: SchweiKart, Vicki L.
/ TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors
/ NUMBER OF SEQUENCES: 66
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
/ STREET: 6300 Sears Tower, 233 South Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/299,843A
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 09/088,337
/ FILING DATE: 01-JUN-1998
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/153,848
/ FILING DATE: 17-NOV-1993
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/977,452
/ FILING DATE: 17-NOV-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Jill E. Uh1
/ REGISTRATION NUMBER: 43,213
/ REFERENCE/DOCKET NUMBER: 27866/32059B
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 474-6300
/ TELEFAX: (312) 474-0448
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 44:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 339 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-09-299-843A-44

Query Match      27.0%; Score 483.5; DB 3; Length 339;
Best Local Similarity 34.6%; Pred. No. 2.7e-30;
Matches 115; Conservative 63; Mismatches 129; Indels 25; Gaps 10;
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```
QY      304 LYYFAGENPKDRKLSAL-----RKGHPOKAKTK 331
DB      296 MYFVAEKPRHALCNLLCGKRLKGPSPFEGK 327

RESULT 7
US-09-088-337B-44
/ Sequence 44, Application us/09088337B
/ Patent No. 6348574
/ GENERAL INFORMATION:
/ APPLICANT: Godiska, Ronald
/ APPLICANT: Gray, Patrick W.
/ APPLICANT: SchweiKart, Vicki L.
/ TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
/ NUMBER OF SEQUENCES: 66
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
/ STREET: 6300 Sears Tower, 233 South Wacker Drive
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/088,337B
/ FILING DATE: 01-Jun-1998
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/153,848
/ FILING DATE: 17-NOV-1993
/ APPLICATION NUMBER: US 07/977,452
/ FILING DATE: 17-NOV-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: No. 6348574and, Greta E.
/ REGISTRATION NUMBER: 35,302
/ REFERENCE/DOCKET NUMBER: 31794
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (312) 474-6300
/ TELEFAX: (312) 474-0448
/ TELEX: 25-3856
/ INFORMATION FOR SEQ ID NO: 44:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 339 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-09-088-337B-44

Query Match      27.0%; Score 483.5; DB 3; Length 339;
Best Local Similarity 34.6%; Pred. No. 2.7e-30;
Matches 115; Conservative 63; Mismatches 129; Indels 25; Gaps 10;
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Db      184 -LVR-EKASHHALVSLAVALTPFPITVTCYLLIIRSL-----RQGLRVEKRLKTKAVR 235
      248 TIIITLIFPLCPPLPYHTLTTLTKV--GLCKDLHKALV--ITLALAAANACENPL 303
      236 MIAIVLAIFVCFPVYHNSVYVLAHRSHGASCATRIALANRITSCLTSLNGALDPI 295
Qy      304 LYFFAGENFDRLKSLA---RKGHPOKAKTK 331
      296 MYFFVAEKFRHALCNLLCGKRLKGPPSPFGK 327

```

RESULT 8

```

US-09-170-496D-32
; Sequence 32, Application US/09170496D
; Patent No. 655339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 655339-Endogenous, Constitutively Activated Human G Protein-
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: AEN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-170-496D-32

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```

Query Match      27.0%; Score 483.5; DB 4; Length 339;
Best Local Similarity 34.6%; Pred. No. 2,7e-30;
Matches 115; Conservative 63; Mismatches 129; Indels 25; Gaps 10;

Qy      16 EMBPG---TFSNNNSRNCITEN-FKREFPPIVYLIIFFMGVGLNGLSIVFLQPYKST 71
      5 EVAPPGILTNFSLATACQCOETPLENMLFASFYLLDFILALVGNLTALMLFIRDKSGT 64
      72 SVNVFMLNLASDLPISTLPFRADYYLRGSMIFGDLACRIMSYSLYVMYSSIVFLTV 131
      65 PAVVFLMHLAVADSCVLPTRLVYFSGNHPFGSIACRLGFLFLYLMYASIVFLTC 124
      132 LSVVRFPLAMVHPRLHVTISRSAMILCGIIMLI--MASSIMLDGSGEONGSVTSCL 190
      125 ISADRFLAIVHPYKSLKLRPLVAHLACAFMWVAVAMAPLIVSPQTVQTNHTVCLQ- 163
      191 NLKIAKLQTMNTIALVVGCLLPFTLSICYLIIIRVILKVEVBSGLRVSHR---KALT 247
      184 -LVR-EKASHHALVSLAVALTPFPITVTCYLLIIRSL-----RQGLRVEKRLKTKAVR 235
      248 TIIITLIFPLCPPLPYHTLTTLTKV--GLCKDLHKALV--ITLALAAANACENPL 303
      236 MIAIVLAIFVCFPVYHNSVYVLAHRSHGASCATRIALANRITSCLTSLNGALDPI 295
Qy      304 LYFFAGENFDRLKSLA---RKGHPOKAKTK 331
      296 MYFFVAEKFRHALCNLLCGKRLKGPPSPFGK 327

```

```

RESULT 9
PCT-US93-11153-44
; Sequence 44, Application PC/TUS9311153
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; APPLICANT: Gray, Patrick W.
; APPLICANT: Schenkart, Vicki L.
; TITLE OF INVENTION: Novel Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell

```

```

; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11153
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Noland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 339 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-11153-44

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Query Match      27.0%; Score 483.5; DB 5; Length 339;
Best Local Similarity 34.6%; Pred. No. 2,7e-30;
Matches 115; Conservative 63; Mismatches 129; Indels 25; Gaps 10;

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      72 SVNVFMLNLASDLPISTLPFRADYYLRGSMIFGDLACRIMSYSLYVMYSSIVFLTV 131
      65 PAVVFLMHLAVADSCVLPTRLVYFSGNHPFGSIACRLGFLFLYLMYASIVFLTC 124
      132 LSVVRFPLAMVHPRLHVTISRSAMILCGIIMLI--MASSIMLDGSGEONGSVTSCL 190
      125 ISADRFLAIVHPYKSLKLRPLVAHLACAFMWVAVAMAPLIVSPQTVQTNHTVCLQ- 163
      191 NLKIAKLQTMNTIALVVGCLLPFTLSICYLIIIRVILKVEVBSGLRVSHR---KALT 247
      184 -LVR-EKASHHALVSLAVALTPFPITVTCYLLIIRSL-----RQGLRVEKRLKTKAVR 235
      248 TIIITLIFPLCPPLPYHTLTTLTKV--GLCKDLHKALV--ITLALAAANACENPL 303
      236 MIAIVLAIFVCFPVYHNSVYVLAHRSHGASCATRIALANRITSCLTSLNGALDPI 295
Qy      304 LYFFAGENFDRLKSLA---RKGHPOKAKTK 331
      296 MYFFVAEKFRHALCNLLCGKRLKGPPSPFGK 327

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RESULT 10
PCT-US95-07180-2
; Sequence 2, Application PC/TUS9507180
; GENERAL INFORMATION:
; APPLICANT: Li, Yi
; APPLICANT: GOCAYNE, JEANINE D
; APPLICANT: RUBEN, STEVEN M
; TITLE OF INVENTION: G-PROTEIN RECEPTOR HIBEB69
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, CECCHI,

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ADDRESSER: STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NJ
COUNTRY: US
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07180
FILING DATE: 06-JUNE-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 30,073
REFERENCE/DOCKET NUMBER: 325800-366
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-07180-2

Query Match 27.0%; Score 483.5; DB 5; Length 339;
Best Local Similarity 34.6%; Pred. No. 2,7e-30;
Matches 115; Conservative 63; Mismatches 129; Indels 25; Gaps 10;

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DB 65 PANVFLMLAVDLSCVLPFLVYHFGSNMPPGSIACRLTGFLFYLMNASIYFLTC 124
QY 132 LSVRFPLAMVHPRLLHTSIRSAWILCGIWIIL-MASSIMLDGSGRONGSVTSCTEL 190
DB 125 ISADRFLLAVHPRKSLKRLRPLVLAHACFLMWVAVAMAPLVSPQTVQTNHTVCLQ- 183
QY 191 NLKXIAKQTMNYIALVVGCLLPFFTLISCYLLIRVLLKVEVPESGLRVSHR---KALT 247
DB 184 -LYR-EKASHMALVSLAVAFTEPFFITVTCYLLIIRSL-----RQGLRVEKRLTKAVR 235
QY 248 TITITLIIFFLCPLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAANAACFNL 303
DB 236 MAIVLAIFLVCFVPHVNRSVYVLAHRSHGASCATORILALANRITSLTSLNGALDEI 295
QY 304 LYFAGENFKDLKSLA---RKGHPOKAKTK 331
DB 296 MYFVAEKFRHALCNILCGRLKGPSPSEK 327

RESULT 11
US-09-170-496D-182
Sequence 182, Application US/09170496D
Patent No. 6555339
GENERAL INFORMATION:
APPLICANT: Behan, Dominic P.
APPLICANT: Chalmers, Derek T.
TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
FILE REFERENCE: AREN-0040
CURRENT APPLICATION NUMBER: US/09170,496D
FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 294

SOFTWARE: Patentin version 3.1
SEQ ID NO 182
LENGTH: 339
TYPE: PRT
ORGANISM: Homo sapiens
US-09-170-496D-182

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Best Local Similarity 34.6%; Pred. No. 4,6e-30;
Matches 115; Conservative 62; Mismatches 130; Indels 25; Gaps 10;

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QY 72 SVNVFLMLALISDLFIPTLPFRADYYLIGSNMIFGDLACRIMSYSLVNMYSIYFLTV 131
DB 65 PANVFLMLAVDLSCVLPFLVYHFGSNMPPGSIACRLTGFLFYLMNASIYFLTC 124
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QY 191 NLKXIAKQTMNYIALVVGCLLPFFTLISCYLLIRVLLKVEVPESGLRVSHR---KALT 247
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QY 248 TITITLIIFFLCPLPYHTLRTVHLTTWKV--GLCKDRLHKALV--ITLALAANAACFNL 303
DB 236 MAIVLAIFLVCFVPHVNRSVYVLAHRSHGASCATORILALANRITSLTSLNGALDEI 295
QY 304 LYFAGENFKDLKSLA---RKGHPOKAKTK 331
DB 296 MYFVAEKFRHALCNILCGRLKGPSPSEK 327

RESULT 12
US-08-513-974B-374
Sequence 374, Application US/08513974B
Patent No. 614139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohkaki, Tetsuya
APPLICANT: Fukumui, Shoji
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSER: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:

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Oy      74 NVFMNLIALSIDLLFSTLPPFRADYYLRGSNWIPEGDLACRINSYSLYVMNYSIYFLTVLS  133
Db      76 SYVMENLIALAFLLYVLTLPALFIYFYNKTDWIFGVMCKLQRFIHWNLVGSILFLFTGIS  135

Oy      134 VVRFILAWHPRLRLVHTSIRSAMIICGIIWIIIMASSIMLL--DSGEONGSVSCLE-  189
Db      136 VHRITGVVHPLKSLGRLLKGGAAVYSSLYMALVAVIAPILFYSGISGRKKITII-CYDT  194

Oy      190 -----LNIYKIAKLTQNNYIALVWGCLLPFTLSICYLLIIRVLKVEVPESGELVSHRK  244
Db      195 TADEYLRSYSPVYSMCTIVFMFCI-----PFYIILCCYGIYKALLYKOLDNSPLR--RK  246

Oy      245 ALTTIILILIFELCFELPYHTLRVHL-----TTKRGGLCDRIHLKALVTITLAAANA  298
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US-08-781-250-2

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Oy      60 IYFLOPYKXSTVNNPMLMLAISDLFIPTSLPFRADYLRGSSNMFEDLACRINSYSIX 119
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Oy      120 VNMWSSYFLPTVSVVRFLAMVHPRLHTVTSIRSAMILCGIIMILIMSSJML-LDSGS 178
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Oy      179 EQNGSVTSCLEMLYKIAK--LOTNMYIALVYGCCLPFTLSICYLLIRVLLKRVBPVS 236
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Oy      237 GLRVSHRKATTTTIIITLIFLFCFLRPHYRLATVLLTMTWVGCK--DELHRAVL-ITLA 292
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Oy      293 LAAANACPNPLLYYPAGENPKD-----RLKSALRKHPQAK 329
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 17:52:40 ; Search time 148 Seconds

(Without alignments)
835.025 Million cell updates/sec

Title: US-09-980-049-1

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1788	100.0	346	US-09-826-791-6	Sequence 6, Appl1
2	1788	100.0	346	US-09-866-230-7	Sequence 7, Appl1
3	1788	100.0	346	US-09-866-230-9	Sequence 9, Appl1
4	1788	100.0	346	US-09-828-478-2	Sequence 2, Appl1
5	1788	100.0	346	US-09-779-679-2	Sequence 2, Appl1
6	1788	100.0	346	US-09-779-679-26	Sequence 26, Appl1
7	1788	100.0	346	US-09-891-225-30	Sequence 30, Appl1
8	1788	100.0	346	US-09-980-049-1	Sequence 1, Appl1
9	1788	100.0	346	US-10-225-567A-589	Sequence 589, Appl1
10	1788	100.0	346	US-10-349-021-2	Sequence 2, Appl1
11	1788	100.0	346	US-10-321-807-14	Sequence 14, Appl1
12	1788	100.0	346	US-10-131-332A-2	Sequence 2, Appl1
13	1788	100.0	346	US-10-369-405-30	Sequence 30, Appl1

14	1788	100.0	346	US-10-182-605-2	Sequence 2, Appl1
15	1788	100.0	346	US-10-403-161-22	Sequence 22, Appl1
16	1788	100.0	346	US-10-403-161-24	Sequence 24, Appl1
17	1788	100.0	346	US-10-343-650A-58	Sequence 58, Appl1
18	1788	100.0	346	US-10-297-247-2	Sequence 2, Appl1
19	1788	100.0	346	US-10-321-807-14	Sequence 14, Appl1
20	1788	100.0	346	US-10-314-048A-14	Sequence 14, Appl1
21	1788	100.0	346	US-10-757-262-40	Sequence 40, Appl1
22	1782	99.7	346	US-10-321-807-88	Sequence 88, Appl1
23	1782	99.7	346	US-10-321-807-88	Sequence 88, Appl1
24	1782	99.7	346	US-10-314-048A-88	Sequence 88, Appl1
25	1782	98.5	341	US-09-991-225-55	Sequence 55, Appl1
26	1762	98.5	341	US-10-369-405-55	Sequence 55, Appl1
27	1712	95.7	330	US-09-826-791-2	Sequence 2, Appl1
28	1712	95.7	330	US-09-991-225-2	Sequence 2, Appl1
29	1712	95.7	330	US-10-369-405-2	Sequence 2, Appl1
30	1712	95.7	330	US-10-775-965-110	Sequence 110, Appl1
31	612	34.2	126	US-10-296-115-1356	Sequence 1356, Appl1
32	564	31.5	337	US-10-290-078-21	Sequence 21, Appl1
33	559	31.3	337	US-09-866-230-8	Sequence 8, Appl1
34	559	31.3	337	US-09-828-478-5	Sequence 5, Appl1
35	559	31.3	337	US-09-779-679-27	Sequence 27, Appl1
36	559	31.3	337	US-09-991-225-6	Sequence 6, Appl1
37	559	31.3	337	US-10-055-106C-3	Sequence 3, Appl1
38	559	31.3	337	US-10-225-567A-547	Sequence 547, Appl1
39	559	31.3	337	US-10-349-021-5	Sequence 5, Appl1
40	559	31.3	337	US-10-369-405-6	Sequence 6, Appl1
41	559	31.3	337	US-10-692-605-4	Sequence 4, Appl1
42	557	31.2	337	US-10-167-192-3	Sequence 3, Appl1
43	557	31.2	337	US-10-400-991-6	Sequence 6, Appl1
44	487.5	27.3	337	US-09-943-198-4	Sequence 4, Appl1
45	487.5	27.3	337	US-09-885-453-1	Sequence 1, Appl1

ALIGNMENTS

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RESULT 1
US-09-826-791-6
; Sequence 6, Application US/09826791
; Patent No. US20010039037A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Inc
; TITLE OF INVENTION: NO. US20010039037A1 Polypeptide
; FILE REFERENCE: P010914ADAM
; CURRENT APPLICATION NUMBER: US/09/826,791
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 0008504.3
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/198,367
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-826-791-6

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Query Match 100.0%; Score 1788; DB 9; Length 346;
Best Local Similarity 100.0%; Pred. No. 3e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 YVFLQYKSTSVNFMALISDLFIPTLPFRADYLRGSWITGDLACRIMSYSLV 120
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Db 61 YVFLQYKSTSVNFMALISDLFIPTLPFRADYLRGSWITGDLACRIMSYSLV 120
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Db 121 NMYSSIFLTVLSVRFAMVHFRLLVHTSIRSAMILGIIWILIMASSIMLDSGSEQ 180
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RESULT 2
US-09-866-230-7
; Sequence 7, Application US/09866230
; Patent No. US20020150901A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Andrew, et al.
; TITLE OF INVENTION: No. US20020150901A1e1 Nucleic Acids, Polypeptides, Methods of Mak
; FILE REFERENCE: REG 771A
; CURRENT APPLICATION NUMBER: US/09/866,230
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/207,725
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7
; LENGTH: 346
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-866-230-7

Query Match 100.0%; Score 1788; DB 9; Length 346;
Best Local Similarity 100.0%; Pred. No. 3e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-866-230-9
; Sequence 9, Application US/09866230
; Patent No. US20020150901A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Andrew, et al.
; TITLE OF INVENTION: No. US20020150901A1e1 Nucleic Acids, Polypeptides, Methods of Mak
; FILE REFERENCE: REG 771A
; CURRENT APPLICATION NUMBER: US/09/866,230

; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/207,725
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 9
; LENGTH: 346
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-866-230-9

Query Match 100.0%; Score 1788; DB 9; Length 346;
Best Local Similarity 100.0%; Pred. No. 3e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 301 NPLLYYFAGENFKDRLKSALRKGHPOKATKCVFVSVWLKRETRV 346

RESULT 4
US-09-828-478-2
; Sequence 2, Application US/09828478
; Patent No. US20020155528A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
; FILE REFERENCE: 04974.00458
; CURRENT APPLICATION NUMBER: US/09/828,478
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,196
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/254,876
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-828-478-2

Query Match 100.0%; Score 1788; DB 9; Length 346;
Best Local Similarity 100.0%; Pred. No. 3e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKFMSLQPSISVSSEMENGTFSSNNRNCTIENFKKEFPPIVYLIIFPMGVLAGNGLSI 60
Db 1 MERKFMSLQPSISVSSEMENGTFSSNNRNCTIENFKKEFPPIVYLIIFPMGVLAGNGLSI 60
QY 61 YVFLOPKKSTSVNVFMNLAIISDLFIETLPFRADYYIRGSNWIFGDLACRIMSYSLVY 120

Db 61 YVFLQPYKSTSVNVFNLALISDLFIPTLPFRADYYLRGNSWIFGDLACRIMSYSLV 120
QY 121 NMYSIYFLTVLSVVRFLAVHPRLHVTISRSAMILCGIIMLMASSIMLDGSEQ 180
Db 121 NMYSIYFLTVLSVVRFLAVHPRLHVTISRSAMILCGIIMLMASSIMLDGSEQ 180
QY 181 NGVTSCLBLNKIKAKLQTMNYIALVVGCLPFTLSICYLLIIRVLKVEVPEGSLRV 240
Db 181 NGVTSCLBLNKIKAKLQTMNYIALVVGCLPFTLSICYLLIIRVLKVEVPEGSLRV 240
QY 241 SHRKALTTIIITLIIFLFCFLPYHTLRVTLTWKVGCLCKDRHLKALVITLALAAACF 300
Db 241 SHRKALTTIIITLIIFLFCFLPYHTLRVTLTWKVGCLCKDRHLKALVITLALAAACF 300
QY 301 NPLIYFAGENFMDRLKSALRKHPQAKTKCVFVSWLRKETRV 346
Db 301 NPLIYFAGENFMDRLKSALRKHPQAKTKCVFVSWLRKETRV 346

RESULT 5

US-09-779-679-2
Sequence 2, Application US/09779679
Publication No. US20030082757A1
GENERAL INFORMATION:
APPLICANT: Taupier, Raymond J
APPLICANT: Burgess, Catherine E
APPLICANT: Padigaru, Muralidhara
APPLICANT: Tchiernev, Velizar T
APPLICANT: Mishra, Vishnu S
APPLICANT: Casman, Stacie
APPLICANT: Ballinger, Robert
APPLICANT: Vermet, Corine A
APPLICANT: Li, Li
APPLICANT: Spytek, Kimberly A
APPLICANT: Andrew, David P
APPLICANT: Mezes, Peter S
TITLE OF INVENTION: No. US20030082757A1 Proteins and Nucleic Acids Encoding the Sam
FILE REFERENCE: 15966-661
CURRENT APPLICATION NUMBER: US/09/779, 679
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: USSN 60/181045
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: USSN 60/181391
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: USSN 60/180, 929
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: USSN 60/219758
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: USSN 60/181339
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: USSN 60/181344
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: USSN 60/221341
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: USSN 60/181392
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: USSN 60/219585
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: USSN 60/181157
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens
US-09-779-679-2

Query Match 100.0%; Score 1788; DB 10; Length 346;
Best Local Similarity 100.0%; Pctd. No. 3e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MERKFMLOPSISVSEMEPMTGTFNNNSRNCIENFKREFPIYVLIIFPMGVLGNGLSI 60

Db 1 MERKFMLOPSISVSEMEPMTGTFNNNSRNCIENFKREFPIYVLIIFPMGVLGNGLSI 60
QY 61 YVFLQPYKSTSVNVFNLALISDLFIPTLPFRADYYLRGNSWIFGDLACRIMSYSLV 120
Db 61 YVFLQPYKSTSVNVFNLALISDLFIPTLPFRADYYLRGNSWIFGDLACRIMSYSLV 120
QY 121 NMYSIYFLTVLSVVRFLAVHPRLHVTISRSAMILCGIIMLMASSIMLDGSEQ 180
Db 121 NMYSIYFLTVLSVVRFLAVHPRLHVTISRSAMILCGIIMLMASSIMLDGSEQ 180
QY 181 NGVTSCLBLNKIKAKLQTMNYIALVVGCLPFTLSICYLLIIRVLKVEVPEGSLRV 240
Db 181 NGVTSCLBLNKIKAKLQTMNYIALVVGCLPFTLSICYLLIIRVLKVEVPEGSLRV 240
QY 241 SHRKALTTIIITLIIFLFCFLPYHTLRVTLTWKVGCLCKDRHLKALVITLALAAACF 300
Db 241 SHRKALTTIIITLIIFLFCFLPYHTLRVTLTWKVGCLCKDRHLKALVITLALAAACF 300
QY 301 NPLIYFAGENFMDRLKSALRKHPQAKTKCVFVSWLRKETRV 346
Db 301 NPLIYFAGENFMDRLKSALRKHPQAKTKCVFVSWLRKETRV 346

RESULT 6

US-09-779-679-26
Sequence 26, Application US/09779679
Publication No. US20030082757A1
GENERAL INFORMATION:
APPLICANT: Taupier, Raymond J
APPLICANT: Burgess, Catherine E
APPLICANT: Padigaru, Muralidhara
APPLICANT: Tchiernev, Velizar T
APPLICANT: Mishra, Vishnu S
APPLICANT: Casman, Stacie
APPLICANT: Ballinger, Robert
APPLICANT: Vermet, Corine A
APPLICANT: Li, Li
APPLICANT: Spytek, Kimberly A
APPLICANT: Andrew, David P
APPLICANT: Mezes, Peter S
TITLE OF INVENTION: No. US20030082757A1 Proteins and Nucleic Acids Encoding the Sai
FILE REFERENCE: 15966-661
CURRENT APPLICATION NUMBER: US/09/779, 679
PRIOR FILING DATE: 2001-02-08
PRIOR APPLICATION NUMBER: USSN 60/181045
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: USSN 60/181391
PRIOR FILING DATE: 2000-02-17
PRIOR APPLICATION NUMBER: USSN 60/180, 929
PRIOR FILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: USSN 60/219758
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: USSN 60/181339
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: USSN 60/181344
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: USSN 60/221341
PRIOR FILING DATE: 2000-07-26
PRIOR APPLICATION NUMBER: USSN 60/181392
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: USSN 60/219585
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: USSN 60/181157
PRIOR FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 26
LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens
US-09-779-679-26

Query Match 100.0%; Score 1788; DB 10; Length 346;
 Best Local Similarity 100.0%; Pred. No. 3e-148;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKFMSLQPSISVSSEMEPNGTFSNNNSRNCCTIENFKREPFPIVYLIIFPWGVLGNGLSI 60
 DB 1 MERKFMSLQPSISVSSEMEPNGTFSNNNSRNCCTIENFKREPFPIVYLIIFPWGVLGNGLSI 60

QY 61 YVFLQPYKSTSVNVFNLALISDLFIPTLPFRADYILRGSNWIFGDLACRIMSYSLYV 120
 DB 61 YVFLQPYKSTSVNVFNLALISDLFIPTLPFRADYILRGSNWIFGDLACRIMSYSLYV 120

QY 121 NMYSIYFLTVLSVVRFLAMVHPFRLHVTIRSAMILGIIWILIMASSIMLDSGSEQ 180
 DB 121 NMYSIYFLTVLSVVRFLAMVHPFRLHVTIRSAMILGIIWILIMASSIMLDSGSEQ 180

QY 181 NGSVTSCEBLNLYKIAKQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEVPESGLRV 240
 DB 181 NGSVTSCEBLNLYKIAKQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEVPESGLRV 240

QY 241 SHRKALTTITITLIIFLFCPLPYHTLRVHTLTWKVGLCKDRLHKAIVTTLAANAACF 300
 DB 241 SHRKALTTITITLIIFLFCPLPYHTLRVHTLTWKVGLCKDRLHKAIVTTLAANAACF 300

QY 301 NPLLYFAGENFKDLKSLARKGHPQAKTKCVFPVSVMLRKETRV 346
 DB 301 NPLLYFAGENFKDLKSLARKGHPQAKTKCVFPVSVMLRKETRV 346

RESULT 7
 US-09-991-225-30
 ; Sequence 30, Application US/09991225
 ; Publication No. US20030153063A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPBMY11, EXPRESSED HT
 ; FILE REFERENCE: D0075.NP
 ; CURRENT APPLICATION NUMBER: US/09/991,225
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/249,613
 ; PRIOR FILING DATE: 2000-11-17
 ; PRIOR APPLICATION NUMBER: 60/257,611
 ; PRIOR FILING DATE: 2000-12-21
 ; PRIOR APPLICATION NUMBER: 60/305,818
 ; PRIOR FILING DATE: 2001-07-16
 ; NUMBER OF SEQ ID NOS: 81
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 30
 ; LENGTH: 346
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-991-225-30

Query Match 100.0%; Score 1788; DB 10; Length 346;
 Best Local Similarity 100.0%; Pred. No. 3e-148;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKFMSLQPSISVSSEMEPNGTFSNNNSRNCCTIENFKREPFPIVYLIIFPWGVLGNGLSI 60
 DB 1 MERKFMSLQPSISVSSEMEPNGTFSNNNSRNCCTIENFKREPFPIVYLIIFPWGVLGNGLSI 60

QY 61 YVFLQPYKSTSVNVFNLALISDLFIPTLPFRADYILRGSNWIFGDLACRIMSYSLYV 120
 DB 61 YVFLQPYKSTSVNVFNLALISDLFIPTLPFRADYILRGSNWIFGDLACRIMSYSLYV 120

QY 121 NMYSIYFLTVLSVVRFLAMVHPFRLHVTIRSAMILGIIWILIMASSIMLDSGSEQ 180
 DB 121 NMYSIYFLTVLSVVRFLAMVHPFRLHVTIRSAMILGIIWILIMASSIMLDSGSEQ 180

QY 181 NGSVTSCEBLNLYKIAKQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEVPESGLRV 240
 DB 181 NGSVTSCEBLNLYKIAKQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEVPESGLRV 240

QY 241 SHRKALTTITITLIIFLFCPLPYHTLRVHTLTWKVGLCKDRLHKAIVTTLAANAACF 300
 DB 241 SHRKALTTITITLIIFLFCPLPYHTLRVHTLTWKVGLCKDRLHKAIVTTLAANAACF 300

QY 301 NPLLYFAGENFKDLKSLARKGHPQAKTKCVFPVSVMLRKETRV 346
 DB 301 NPLLYFAGENFKDLKSLARKGHPQAKTKCVFPVSVMLRKETRV 346

RESULT 8
 US-09-980-049-1
 ; Sequence 1, Application US/09980049
 ; Publication No. US20040220092A1
 ; GENERAL INFORMATION:
 ; APPLICANT: INCYTE GENOMICS, INC.
 ; APPLICANT: POLICKY, Jennifer L.
 ; APPLICANT: TRIBOULEY, Catherine M.
 ; APPLICANT: TANG, Y. Tom
 ; APPLICANT: BAUGHN, Mariah R.
 ; APPLICANT: GRAUL, Richard
 ; APPLICANT: KHAN, Fairah A.
 ; APPLICANT: NGUYEN, Danielle B.
 ; APPLICANT: PATTERSON, Chandra
 ; APPLICANT: LAL, Preeti
 ; APPLICANT: AU-YOUNG, Janice
 ; APPLICANT: YANG, Junming
 ; APPLICANT: HAPALIA, April
 ; APPLICANT: WALIA, Nandinder K.
 ; APPLICANT: DAS, Debopriya
 ; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
 ; FILE REFERENCE: PI-0072 PCT
 ; CURRENT APPLICATION NUMBER: US/09/980,049
 ; PRIOR FILING DATE: 2001-11-28
 ; PRIOR APPLICATION NUMBER: 60/193,051; 60/195,155; 60/199,084; 60/200,551; 60/202,278
 ; PRIOR FILING DATE: 2000-03-29; 2000-04-06; 2000-04-20; 2000-04-28; 2000-05-05
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 1
 ; LENGTH: 346
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No: 5628963CD1
 ; US-09-980-049-1

Query Match 100.0%; Score 1788; DB 12; Length 346;
 Best Local Similarity 100.0%; Pred. No. 3e-148;
 Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKFMSLQPSISVSSEMEPNGTFSNNNSRNCCTIENFKREPFPIVYLIIFPWGVLGNGLSI 60
 DB 1 MERKFMSLQPSISVSSEMEPNGTFSNNNSRNCCTIENFKREPFPIVYLIIFPWGVLGNGLSI 60

QY 61 YVFLQPYKSTSVNVFNLALISDLFIPTLPFRADYILRGSNWIFGDLACRIMSYSLYV 120
 DB 61 YVFLQPYKSTSVNVFNLALISDLFIPTLPFRADYILRGSNWIFGDLACRIMSYSLYV 120

QY 121 NMYSIYFLTVLSVVRFLAMVHPFRLHVTIRSAMILGIIWILIMASSIMLDSGSEQ 180
 DB 121 NMYSIYFLTVLSVVRFLAMVHPFRLHVTIRSAMILGIIWILIMASSIMLDSGSEQ 180

QY 181 NGSVTSCEBLNLYKIAKQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEVPESGLRV 240
 DB 181 NGSVTSCEBLNLYKIAKQTMNYIALVVGCLLPFTLSICYLLIIRVLKVEVPESGLRV 240

QY 241 SHRKALTTITITLIIFLFCPLPYHTLRVHTLTWKVGLCKDRLHKAIVTTLAANAACF 300
 DB 241 SHRKALTTITITLIIFLFCPLPYHTLRVHTLTWKVGLCKDRLHKAIVTTLAANAACF 300

QY 301 NPLLYFAGENFKDLKSLARKGHPQAKTKCVFPVSVMLRKETRV 346
 DB 301 NPLLYFAGENFKDLKSLARKGHPQAKTKCVFPVSVMLRKETRV 346

Db 301 NPLLYFAGENFKDRLKSLARKGHPQAKTKCVFPVSVWLKRETRV 346

RESULT 9
US-10-225-567A-589
; Sequence 589, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 589
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-589

Query Match 100.0%; Score 1788; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 3e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKFNLSLOPSISVSEMEPNGTFSNNNSRNCITENFKRBPPIYVLIIFPMGVANGLSI 60
Db 1 MERKFNLSLOPSISVSEMEPNGTFSNNNSRNCITENFKRBPPIYVLIIFPMGVANGLSI 60

QY 61 YVFLQPKKSTSVNVFNLALISDLPISTLPFRADYYLRGNSWIFGDLACRIMSYSLV 120
Db 61 YVFLQPKKSTSVNVFNLALISDLPISTLPFRADYYLRGNSWIFGDLACRIMSYSLV 120

QY 121 NMTSSIFLTVLSVVRFLAMVHPRLHVTISIRSAWILCGIWIILMASSIMLLDGSSEQ 180
Db 121 NMTSSIFLTVLSVVRFLAMVHPRLHVTISIRSAWILCGIWIILMASSIMLLDGSSEQ 180

QY 181 NGSVTSCLELNLYKIAKQTMNTIALVVGCLPFTLSICYLIRVLLKVEPESGLRV 240
Db 181 NGSVTSCLELNLYKIAKQTMNTIALVVGCLPFTLSICYLIRVLLKVEPESGLRV 240

QY 241 SHRKALTTIIITLIIFLCPYHTLRVHLLTWKVGCLCKDRHLKALVITLALAAACF 300
Db 241 SHRKALTTIIITLIIFLCPYHTLRVHLLTWKVGCLCKDRHLKALVITLALAAACF 300

QY 301 NPLLYFAGENFKDRLKSLARKGHPQAKTKCVFPVSVWLKRETRV 346
Db 301 NPLLYFAGENFKDRLKSLARKGHPQAKTKCVFPVSVWLKRETRV 346

RESULT 10
US-10-349-021-2
; Sequence 2, Application US/10349021
; Publication No. US20030157541A1
; GENERAL INFORMATION:
; APPLICANT: Xiao, Yonghong
; TITLE OF INVENTION: Regulation of Human CysLT2-Like GPCR
; FILE REFERENCE: 04974, 00458
; CURRENT APPLICATION NUMBER: US/10/349,021
; PRIOR FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: US/09/828,478
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/195,196
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 60/254,876
; PRIOR FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-349-021-2

Query Match 100.0%; Score 1788; DB 14; Length 346;
Best Local Similarity 100.0%; Pred. No. 3e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKFNLSLOPSISVSEMEPNGTFSNNNSRNCITENFKRBPPIYVLIIFPMGVANGLSI 60
Db 1 MERKFNLSLOPSISVSEMEPNGTFSNNNSRNCITENFKRBPPIYVLIIFPMGVANGLSI 60

QY 61 YVFLQPKKSTSVNVFNLALISDLPISTLPFRADYYLRGNSWIFGDLACRIMSYSLV 120
Db 61 YVFLQPKKSTSVNVFNLALISDLPISTLPFRADYYLRGNSWIFGDLACRIMSYSLV 120

QY 121 NMTSSIFLTVLSVVRFLAMVHPRLHVTISIRSAWILCGIWIILMASSIMLLDGSSEQ 180
Db 121 NMTSSIFLTVLSVVRFLAMVHPRLHVTISIRSAWILCGIWIILMASSIMLLDGSSEQ 180

QY 181 NGSVTSCLELNLYKIAKQTMNTIALVVGCLPFTLSICYLIRVLLKVEPESGLRV 240
Db 181 NGSVTSCLELNLYKIAKQTMNTIALVVGCLPFTLSICYLIRVLLKVEPESGLRV 240

QY 241 SHRKALTTIIITLIIFLCPYHTLRVHLLTWKVGCLCKDRHLKALVITLALAAACF 300
Db 241 SHRKALTTIIITLIIFLCPYHTLRVHLLTWKVGCLCKDRHLKALVITLALAAACF 300

QY 301 NPLLYFAGENFKDRLKSLARKGHPQAKTKCVFPVSVWLKRETRV 346
Db 301 NPLLYFAGENFKDRLKSLARKGHPQAKTKCVFPVSVWLKRETRV 346

RESULT 11
US-10-321-807-14
; Sequence 14, Application US/10321807
; Publication No. US20030166148A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruyong
; APPLICANT: Lowitz, Kevin P.
; TITLE OF INVENTION: No. US20030166148A1-Endogenous, Constitutively Activated Human G
; FILE REFERENCE: AREN0086
; CURRENT APPLICATION NUMBER: US/10/321,807
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US/09/714,008
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: PCT/US99/23938
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: 60/166,088
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,099
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/166,369
; PRIOR FILING DATE: 1999-11-17
; PRIOR APPLICATION NUMBER: 60/171,902
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,901
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/171,900
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/181,749
; PRIOR FILING DATE: 2000-02-11
; Remaining prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14


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; CURRENT APPLICATION NUMBER: US/10/182,605
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: GB 0003079.1
; PRIOR FILING DATE: 2000-02-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-182-605-2

Query Match          100.0%; Score 1788; DB 15; Length 346;
Best Local Similarity 100.0%; Pred. No. 3e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKFMSLQPSISVSEMEPNGTFSNNNSRNCTIENFKREFPIYVLIIFPMGVLAGNLSI 60
DB 1 MERKFMSLQPSISVSEMEPNGTFSNNNSRNCTIENFKREFPIYVLIIFPMGVLAGNLSI 60
QY 61 YVFLQPYKSTSVNFMNLAIISDLFI STLPRADYYLRGSNWI FGDLCRIMSYSLYV 120
DB 61 YVFLQPYKSTSVNFMNLAIISDLFI STLPRADYYLRGSNWI FGDLCRIMSYSLYV 120
QY 121 NMYSIYFLTVLSVRFLLAMVHPRLLHVTISRSAWILCGIWIWLMASIMLDSGSEQ 180
DB 121 NMYSIYFLTVLSVRFLLAMVHPRLLHVTISRSAWILCGIWIWLMASIMLDSGSEQ 180
QY 181 NGSVTSCLEINLYKIAKQTMNYIALVGCILPFTLSICYLLIIRVLKVEVPESGLRV 240
DB 181 NGSVTSCLEINLYKIAKQTMNYIALVGCILPFTLSICYLLIIRVLKVEVPESGLRV 240
QY 241 SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRHLKALVITLALAAANACF 300
DB 241 SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRHLKALVITLALAAANACF 300
QY 301 NPILYYPAGENFDRKLSALRKHPQAKTKCVFVSWMLRKETRV 346
DB 301 NPILYYPAGENFDRKLSALRKHPQAKTKCVFVSWMLRKETRV 346

RESULT 15
US-10-403-161-22
; Sequence 22, Application US/10403161
; Publication No. US20040043930A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David et al.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-573C
; CURRENT APPLICATION NUMBER: US/10/403,161
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: 60/370349
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384543
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/370969
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/403748
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/372019
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/374379
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 09/779679
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: 60/181045
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 10/055877
; PRIOR FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262892
; PRIOR FILING DATE: 2001-01-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 173

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; SOFTWARE: CuraSeqLib version 0.1
; SEQ ID NO 22
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-403-161-22

Query Match          100.0%; Score 1788; DB 15; Length 346;
Best Local Similarity 100.0%; Pred. No. 3e-148;
Matches 346; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERKFMSLQPSISVSEMEPNGTFSNNNSRNCTIENFKREFPIYVLIIFPMGVLAGNLSI 60
DB 1 MERKFMSLQPSISVSEMEPNGTFSNNNSRNCTIENFKREFPIYVLIIFPMGVLAGNLSI 60
QY 61 YVFLQPYKSTSVNFMNLAIISDLFI STLPRADYYLRGSNWI FGDLCRIMSYSLYV 120
DB 61 YVFLQPYKSTSVNFMNLAIISDLFI STLPRADYYLRGSNWI FGDLCRIMSYSLYV 120
QY 121 NMYSIYFLTVLSVRFLLAMVHPRLLHVTISRSAWILCGIWIWLMASIMLDSGSEQ 180
DB 121 NMYSIYFLTVLSVRFLLAMVHPRLLHVTISRSAWILCGIWIWLMASIMLDSGSEQ 180
QY 181 NGSVTSCLEINLYKIAKQTMNYIALVGCILPFTLSICYLLIIRVLKVEVPESGLRV 240
DB 181 NGSVTSCLEINLYKIAKQTMNYIALVGCILPFTLSICYLLIIRVLKVEVPESGLRV 240
QY 241 SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRHLKALVITLALAAANACF 300
DB 241 SHRKALTTIIITLIIFFLCFLPYHTLRTVHLTTWKVGLCKDRHLKALVITLALAAANACF 300
QY 301 NPILYYPAGENFDRKLSALRKHPQAKTKCVFVSWMLRKETRV 346
DB 301 NPILYYPAGENFDRKLSALRKHPQAKTKCVFVSWMLRKETRV 346

Search completed: December 13, 2004, 18:05:05
Job time : 149 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 17:43:39 ; Search time 41 Seconds

(without alignments)
811.976 Million cell updates/sec

Title: US-09-980-049-1

Sequence: 1 MEKKMSLQPSISVSEMEPN.....KATKCVFVSVWLKRETRY 346

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	470	26.3	362	2	S33733
2	447.5	25.0	370	2	JC5549
3	447	25.0	308	2	I50241
4	446	24.9	373	2	JC4737
5	442	24.7	373	2	JC4162
6	440	24.6	361	2	B45680
7	436	24.4	344	2	T09508
8	421.5	23.6	373	2	A47556
9	416	23.3	342	2	S13638
10	416	23.3	375	2	A54966
11	409.5	22.9	342	2	A40191
12	406	22.7	420	2	I51667
13	404	22.6	341	2	S63666
14	400.5	22.4	397	2	S66518
15	398	22.3	380	2	I38435
16	397	22.2	341	2	S43252
17	394.5	22.1	355	2	A45177
18	394	22.0	359	2	I48705
19	393	22.0	355	2	I49339
20	391	21.9	328	2	I55450
21	387	21.6	371	2	JC5796
22	382	21.4	371	2	JC5498
23	378.5	21.2	378	2	B55735
24	378	21.1	355	2	JC5067
25	377.5	21.1	365	2	S68679
26	376	21.0	356	2	I49340
27	374.5	20.9	363	2	I57955
28	374.5	20.9	364	2	JN0763
29	374.5	20.9	383	2	S55594

30	373.5	20.9	387	2	I69202	G protein-coupled
31	372.5	20.8	378	2	A55735	G protein-coupled
32	372	20.8	363	2	I57940	somatostatin recep
33	371.5	20.8	365	2	S68208	G protein-coupled
34	367.5	20.6	427	2	S17148	alpha-thrombin rec
35	366.5	20.5	355	2	G02436	chemokine (C-C) re
36	366	20.5	352	2	JN0694	angiotensin II rec
37	363	20.3	359	2	S15403	angiotensin II rec
38	362.5	20.3	369	2	JC2083	somatostatin recep
39	361.5	20.2	352	2	A43113	chemokine (C-C) re
40	360	20.1	432	2	A43448	thrombin receptor
41	359	20.1	363	2	I48261	angiotensin II rec
42	357	20.0	328	2	JC4800	P2Y6 receptor - hu
43	357	20.0	363	2	A49092	angiotensin II rec
44	356.5	19.9	333	2	I65989	G protein-coupled
45	356.5	19.9	361	2	JC5653	G protein-coupled

ALIGNMENTS

RESULT 1

S33733
G protein-coupled receptor - chicken
C/Species: Gallus gallus (chicken)
C/Date: 06-Jan-1995 #sequence_rev1sion 06-Jan-1995 #ext_change 09-Jul-2004
C/Accession: S33733
R/Webb, T.B.; Simon, J.; Kriehak, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnsto
FEBS Lett. 324, 219-225, 1993
A/Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.
A/Reference number: S33733, PMID:93285340; PMID:8508924
A/Status: preliminary
A/Accession: S33733
A/Molecule type: mRNA
A/Residues: 1-362 <MEB>
A/Cross-references: UNIPROT:P34996; EMBL:X73268; NID:G395084; PID:CA51716.1; PID:G395
C/Superfamily: ATP receptor P2U
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 26.3%; Score 470; DB 2; Length 362;

Best local Similarity 30.6%; Pred. No. 6.1e-31;
Matches 99; Conservative 84; Mismatches 115; Indels 26; Gaps 7;

QY	16	EMENPTFSNNNSRNCCT--ENFKREFPIVYLIIFKGVGLNGLSIVFLQPKKSTSV 73
DB	16	ELIAGGMAAGNATTKSLTGTGFYLLPTVYLVITFTGLNLSVAIMFVFHMRPWSGI 75
QY	74	NVEMLNLSIDLIETLPFRADYLRGSMIFGDLACRIMSYSLVNMWSSIVPTVVS 133
DB	76	SVYMFNLADPLFYVLTLPALIFRYFNKTDWIFGDVCKLQRTIFHVNLYGSLIFLCIS 135
QY	134	VVEFLAMVHPRLIHTYSIRSAWILGIIWILIMASSIML--DSGSBQNSVTSCLR 189
DB	136	VHRVTVGVNPLKSLGRKKKNAYVSSIVMALVAVNIAPILFSGVGRNKKIT--CYDT 194
QY	190	-----LNLKYIAKLQTMNTIALVVGCLLPFTLSICYLLIRVLLKVEYVDSGLRYSHRK 244
DB	195	TADVYRSYFVSVSMCTVTFMFCI-----PFIVILGCGYIIVKXLIYKIDLNSPLR--RK 246
QY	245	ALTTIITLIIPLCLPYHTLTATVH-----TTMKVGLGCRKALKAIVITLAAANA 298
DB	247	SYLVITIVLVFVAVSYLPFVMTLNLRLARLDFOTQPMCAFNDKVATYATQVTRGLASNS 306
QY	299	CENPLIYFAGENFKDLKLSALRK 322
DB	307	CVDPIIYFLAGDFFRRRLRSATRK 330

RESULT 2

JC5549
heptahelical P2Y5-like receptor - human
C/Species: Homo sapiens (man)
C/Date: 02-Sep-1997 #sequence_rev1sion 05-Sep-1997 #ext_change 09-Jul-2004

Query Match 25.0%; Score 447; DB 2; Length 308;
Best Local Similarity 35.4%; Pred. No. 3,9e-29;
Matches 105; Conservative 53; Mismatches 119; Indels 20; Gaps 8;

F.133-153/Domain: transmembrane #status predicted <TM4>
F.117-201/Domain: transmembrane #status predicted <TM5>
F.227-248/Domain: transmembrane #status predicted <TM6>
F.269-292/Domain: transmembrane #status predicted <TM7>

Query 28 SRNCTIE-NFRKRPFFIVYLIIFFMGVLGSLGYVLAQPKKSTSVNFMALISDLL 86
Db 3 SSNSTSDSRKYTYIGCVFSMVFYGLIANCVAIIYFTPLKRNETTYMMLAISDLL 62
QY 87 FISTLPRADYYLRGSMWIFGDLACRIMSYSLVYNNYSIYFTVLISVAFILAMVHPRL 146
Db 63 FVFTLPRFRI-YVFFVRNMPFGVDLCKISVTLFTNNWYSLFPTCISVDFLAIVHPRS 121
QY 147 LHTSISANMILGCIITILMASST--MLDGSSEONGSVTSCLENLKYIKLQTMAY 203
Db 122 KLTATKRNARIVCAVWITVLAGSTPASFPQSTNRQNNRQRCFB-NPESEYWKTYLSR 180
QY 204 IAL---VVGCLLPRFPLSLICYLLIIRVLIVAEYBESGLARSHRKALTTIITLIFPLCP 260
Db 181 IVTIEIVGFPIILNVTGTSWLRKLNK-PLTISRNKSKKKVLMIFVHLVIFCFP 239
QY 261 LPYH-----TLRTVALTTWKVGLCKDRLHKALVITLALAAANCFNPDLIYYPAGE 310
Db 240 VPFVITILIVSWKRT--QTWINGSVVTAVRMYPTVLTCAVNGCFDPFIYYFTSD 293

RESULT 4

G protein-coupled receptor P2Y1 - human
J04737
N.Alternate names: P2Y1 purinergic receptor; P2Y1 purinoceptor
C.Species: Homo sapiens (man)
C.Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C.Accession: J04737; J04615; S54253
R.Janssens, R.; Commun, D.; Piroton, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M.
Biochem. Biophys. Res. Commun. 221, 588-593, 1996
A.Title: Cloning and tissue distribution of the human P2Y1 receptor.
A.Reference number: J04737, MUID:96205320; PMID:8630005
A.Accession: J04737
A.Molecule type: DNA
A.Residues: 1-373 <JAN>
R.Ayyanathan, K.; Webb, T.E.; Sandhu, A.K.; Ahsan, R.S.; Barnard, E.A.; Kunapuli, S.P.
Biochem. Biophys. Res. Commun. 218, 783-788, 1996
A.Title: Cloning and chromosomal localization of the human P2Y1 purinoceptor.
A.Reference number: J04615, MUID:96158962; PMID:8579591
A.Accession: J04615
A.Molecule type: mRNA
A.Residues: 1-373 <AVY>
A.Cross-references: GB:U42029, NID:g1147730, PIDN:AAA97872.1; PID:g1147731
A.Experimental source: erythro leukemia cells
Rileon, C.; Vial, C.; Cazenave, J.; Gachet, C.
submitted to the EMBL Data Library, May 1995
A.Description: Cloning of a human putative P2Y receptor.
A.Reference number: S54253
A.Accession: S54253
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-137,139-373 <LEO>
A.Cross-references: EMBL:249205; NID:g798835; PIDN:CAA89066.1; PID:g798836
C.Comment: This receptor belongs to a family of G protein-coupled receptors. It responds
C.Genetics:
A.Gene: p2Y1; GDB:p2RY1
A.Cross-references: GDB:677125; OMIM:601167
A.Map position: 3pter-3qter
C.Subfamily: ATP receptor P2u
C.Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane prot
F.124-152/Domain: transmembrane #status predicted <TM2>
F.124-152/Domain: transmembrane #status predicted <TM3>


```

Oy      304 LYYFAGENFKDRLKSLARKGHPQAKTYC 332
          ::||::|::|::|::|
Db      292 IYCFELTKKFR--KHLTEKFYSMSRRKC 317

```

RESULT 12

151667
thrombin receptor - African clawed frog
C.Species: *Xenopus laevis* (African clawed frog)
C.Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C.Accession: 151667
R.Gerzsten, R.E.; Chen, J.; Ishii, M.; Ishii, K.; Nanevycz, T.; Turck, C.W.; Vu, T.H.; Q
Nature 368, 648-651, 1994
A.Title: Thrombin receptor's specificity for agonist peptide is determined by its extrac
A.Reference number: 151667; PMID:94195429; PMID:8145852
A.Accession: 151667
A.Status: preliminary; translated from GB/EMBL/DBJ
A.Molecule type: mRNA
A.Residues: 1-420 <GER>
A.Cross-references: UNIPROT:P47749; EMBL:U096332; NID:9495197; PIDD:94951

Query Match 22.7%; Score 406; DB 2; Length 420;
Best Local Similarity 30.9%; Pred. No. 1.2e-25;
Matches 102; Conservative 66; Mismatches 128; Indels 34; Gaps 7;

```

OY 16 MMEPFGTSSNNNS-----RNCIE-----NFKKEFPYVLLIFPFNGVANG 57
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 ELDESGESSGQOAPVPSRARKPIRRNITKEAQYIASSQMLTKFVPSLYTVFVIGLPANT 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 58 LSIYFLOPYKXKTSVNVFVNLNLAISDLFTSTLPPRADYVLRGSNMIFGDLACRIMSYS 117
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 LAIIIFLEPKMKYKRKXPAVVYVMTNLAIADVPFVSVPFKAYHLSGDMVLFEGMGKRIYTAI 180
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 118 LYVNVYSSIFYETLVSVVRFLAMVHPFRLVHTSIRSAMIICGIIWILIMASSITLDSG 177
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 FYCMMYCSVLLIASSVDVRFVAVVYPMHSLSMRMTSRAYMASCFTWLSISTIPLVATE 240
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 178 SEQ--NGSVTSCELENIYKIAKLOTNMYIALVGCGL---PPFTLSICYLLIIRVLK 230
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 241 QTOKIPRLDITTCADVLDKDKOKFYIYFESF--CLLPFVPVPIITTCYIGIIRSLSS 298
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 231 VEVEPSGLRVSHRKALTTIITLIIFCLCPYPYTLRTVHLTTVMKGLCKDRLKALVYT 290
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 299 SSIENS---CKKTRALFLAVVLCVFIICGEPITNVLFLTHY----LQANEFVIFAYILS 351
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 291 LALAAANACFNPDLIYFAGENFKDRLKSAL 320
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 352 ACVGSVSCCLDPLIYYVASSQCORLYSL 381
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 13
S6366
platelet activating factor receptor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S6366
R/Ishii, S.; Matsuda, Y.; Nakamura, M.; Waga, I.; Kume, K.; Izumi, T.; Shimizu, T.
Biochem. J. 314, 671-678, 1996
A/Title: A murine platelet-activating factor receptor gene: cloning, chromosomal localization
A/Reference number: S6366; MUID:96239129; PMID:8670084
A/Accession: S6366
A/Status: Preliminary
A/Molecule type: DNA
A/Residues: 1-341 <ISH>
A/Cross-references: UNIPROT:062035; EMBL:D50872; NID:g1256924; PIDN:BAA09468.1; PID:g1256924
A/Superfamily: ATP receptor P2u

```

	Query Match	22.6%	Score 404;	DB 2;	Length 341;
	Best Local Similarity	30.5%	Pred. No. 1.4e-25;		
	Matches 101; Conservative	66;	Mismatches 134;	Indels 30;	Gaps 10;
OY	17 MEPCGTENNNSRNCTIENFKREPPYYLLIFKGVGLNGLSIVF--LQPKKSTSVN	74			
	:: :: :	:	:: :: :	:: :	:

[illegible]

RESULT 14

566518
proteinase-activated receptor 2 precursor - human
C:Species: Homo sapiens (man)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S66518; S64709; G02131
R:Mytseth, S.; Emilsson, K.; Larsson, A.K.; Strombeck, B.; Sundelin, J.
Eur. J. Biochem. 232, 84-89, 1995
A:Title: Molecular cloning and functional expression of the gene encoding the human prot
A:Reference number: S66518; MUID:96048032; PMID:7556175
A:Accession: S66518
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-397 <UNIS>
A:Cross-references: UNIPROT:P55085; EMBL:Z49993; NID:g1008084; PTDN:CAA90290.1; PID:g100
R:Bohm, S.K.; Kong, W.; Broemme, D.; Smeekens, S.P.; Anderson, D.C.; Connolly, A.; Kahn
Biochem. J. 314, 1009-1016, 1996
A:Title: Molecular cloning, expression and potential functions of the human proteinase-a
A:Reference number: S64709; MUID:9617879; PMID:8615752
A:Accession: S64709
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-137, 'A', 139-397 <BOE>
A:Cross-references: EMBL:U34038; NID:g1041728; PINN:ABA47871.1; PID:g1041729
A:Note: The authors translated the codon GTC for residue 68 as Ile and AAC for residue 2
R:Kahn, M.L.; Coughlin, S.R.
submitted to the EMBL Data Library, September 1995
;Reference number: H00822

Query Match	22.4%	Score 400.5;	DB 2;	Length 397;
Best Local Similarity	30.7%;	Pred. NO. 3.7e-25;		
Matches 99;	Conservative 69;	Mismatches 121;	Indels 33;	Gaps 9

[illegible]

```
Db      137 HGNMWTGECALCNVLIGFPFGNMTCSTLFTCTCLSVORWTVNPMG---HSRKKANIAI 192
      160 GI---IWLIMASSIML-----LDGSEONGSVTSCLBLNLYKIAKLOTMYN-1 204
      193 GISLAIWLLILVLIPIVYVQTIPIPAL-----NITTCADVLPBQLVGMFNYPFL 244
Qy      205 ALVVGCLLPFTTSTICYLIIIRVLKVEVPESGLRVSHRKALTTIIITLIIFLCLPY 263
      245 SLAIGVFLPFAFLPASAYVIMIMLRSSADENSEK-KRKRAIKLIYTVLAMYLICFTPS 303
Db      264 HTLRVHLTTWKVGLCDORLHKALVITLALAAACFNPLLYFAGENFKDRLKSALRKG 323
      304 NLLLVHYFLIK-SQGSHYALYIVALCLSTLNSCIDPFVYFVSHDFRDHAKNALL-- 360
Qy      324 HPQAKTKCVPEVPSVWLRKETR 345
      361 -CRSVRTVKOMQVSLTSKHSR 381
Db
```

RESULT 15

```
138435
angiotensin receptor homolog APJ - human
C:Species: Homo sapiens (man)
C:Date: 15-Mar-1996 #sequence_revision 15-Mar-1996 #text_change 09-Jul-2004
C:Accession: I38435
R/O: Dowd, B.F.; Heiber, M.; Chan, A.; Heng, H.H.; Tsui, L.; Kennedy, J.L.; Shi, X.; Petr
Gene 136, 355-360, 1993
A:Title: A human gene that shows identity with the gene encoding the angiotensin recep
A:Reference number: I38435; MUID:94124031; PMID:8294032
A:Accession: I38435
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-380 <RES>
A:Cross-references: UNIPROT:P35414; EMBL:U03642; NID:G425351; PIDN:AAA18954.1; PID:G4253
A:Gene: APJ
A:Map position: 11q12
A:Intons: #status absent
C:Superfamily: vertebrate rhodopsin
```

```
Query Match      22.3% Score 398; DB 2; Length 380;
Best local Similarity 29.2%; Pred. No. 4.7e-25;
Matches 100; Conservative 71; Mismatches 134; Indels 38; Gaps 13;

Qy      17 MBPNGTFSN-----NSNRCTIENFKRE--FFPIVYLIIFFWGLNGLSIY-VFLQPYKK 69
      1 MEEGDFDNYYGADNQECEYTDWKSSGALIPAIYMLVFLGTTGNGLVLMTVPRSRK 60
Db
Qy      70 STSVNVMMLAIISDLFIITLPPRADYVLRGSMWIFGLACRIMSYSLYNNYSSIYFL 129
      61 RRSADIFIASIAVADLTFVVTLPIMATYRDYDMPGTFCKLSYLIFFVNNYASVFC 120
Db
Qy      130 TVLSVVFELMVPFRLLHTSIRSANILGIIWL--IMASSIML-DSGSEONGSVTS 166
      121 TGLSPDRYLAIVRPNARLRVSGAVAAVAVLALAMPVAVLRTTGDLNNTYKVQ 180
Db
Qy      187 CLBLNLYKIAKLOT-----MNYIALVGLLPFTTSTICYLIIIRVL-----KVEV 233
      181 CY-MDYSMVATVSEMAWEVGLGVSTTVGVVFTIMLCYFPIAQTINAGHPRKERIE- 238
Qy      234 PEGGLRVSHRKALTTIIITLIIFLCLPYHTLRTVH---LTTWKVGLCKDRLHKALVI 289
      239 ---GLR-KRRRLSLIYVAVTFALCMMPYHLYKTLVYMLGSLHMP---CDFDLFLMNIF 291
Db
Qy      290 --TLALAAANACFNPLLYFAGENFKDRLKSALRKGHPQAKT 330
      292 PYCTCISYVNSCLNPLIYAFDFRFRQACTSMLCGGSRCAGT 334
Db
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Search completed: December 13, 2004, 17:53:20
Job time : 42 secs

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